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RESULT 1
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                                                                            Best Local Similarity 100 Matches 309; Conservative
                                                                                                                Query Match
                                                                                                                                                                                                                                                   TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                      CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
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MEDIUM TYPE: 3.5 incl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
                                                                                                                                                                                             LENGTH: 309 amino acids TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/079,029 FILING DATE:
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US-09-136-389-148
US-09-610-838-148
US-09-025-769B-178
US-09-046-028-16
US-08-918-148-79
US-09-646-028-13
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Pred. No. 1.6e-120;
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Result

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Description

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1010 923.5 871 838.5 825 825 811 811 801 804 785.5 776.5 767.5

US-09-079-029-9 US-09-079-029-10 US-09-079-029-11 US-09-260-527-1 US-09-260-527-3 US-10-039-785-53 US-10-039-785-63 US-09-486-814A-2 US-09-486-028-53 US-09-646-028-53 US-09-646-028-53 US-09-646-028-51 US-08-641-04A-75 US-08-918-148-75 US-08-918-148-76 US-08-918-148-77 US-08-918-148-77 US-08-918-148-77 US-08-918-148-77 US-09-188-082-14 US-09-188-082-14 US-09-188-082-14 US-09-364-088-14 US-09-364-088-14 US-09-364-088-14 US-09-488-113B-148 US-08-488-113B-148

9, Appli 11, Appl 1, Appli 1, Appli 3, Appli 40, Appl 40, Appl 53, Appli 55, Appli 55, Appli 55, Appli 75, Appli 76, Appli 8, Appli 8, Appli 8, Appli 8, Appli 10, Appli 11, App

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CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL 120

Post-processing: Minimum Match 08
Maximum Match 10

Maximum Match 100% Listing first 45 summaries

Issued\_Patents\_AA:\*
1: /cgn2\_6/ptodata/1,
2: /cgn2\_6/ptodata/1,
3: /cgn2\_6/ptodata/1,
4: /cgn2\_6/ptodata/1,
5: /cgn2\_6/ptodata/1,
6: /cgn2\_6/ptodata/1,

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/cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
/cgn2\_6/ptodata/1/iaa/Packfiles1.pep:\*

Minimum DB Maximum DB

seq length: 0 seq length: 2000000000

Total number of hits satisfying chosen parameters:

328717 seqs, 42310858 residues

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0

Title: Perfect score:

US-10-052-798-9 1633

MTMITPSFGAFFLEIFNVKK......HHHGAAEQKLISEEDLNGAA 309

Run on: OM protein -

protein search, using sw model

GenCore version Copyright (c) 1993 - 2003

5.1.6 Compugen

September 22, 2003, 15:13:04; Search time 18.2546 Seconds (without alignments) 716.207 Million cell updates/sec

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Patent No.
                                                                                                                      Matches
                                                                                                                                             Query Match
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
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                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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             CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL 120
                          CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL 120
                                                                MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                             MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS 60
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1 DNA Way
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                                                                                                                   Pred. No. 5.1e-107;
8; Mismatches 18;
                                                                                                                                             Score 1460.5;
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Best Local
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                                                                                                                                                                                                                                                               TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winfatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,6
REFERENCE/DOCKET NUMBER:
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CITY: S
                                                                                                                                                                                                                                       LENGTH: 310 amino acids TYPE: Amino Acid
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les 245; Conserv
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                                                                                                  US-09-260-527-3
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Sequence 3, Application US/09260527A
PATENT NO. 6228599
GENERAL INFORMATION:
APPLICANT: KNOX, J.P.
APPLICANT: MILKELSEN, J.D.
APPLICANT: WILLALS, W. G.
TITLE OF INVENTION: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/260, CURRENT APPLICATION NUMBER: US/09/260, CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version SEQ ID NO 1
LENGTH: 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from
OTHER INFORMATION: phage display library known as the Synthetic of
OTHER INFORMATION: Library (#1) from the Centre for Protein
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
-09-260-527-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mikkelsen, J.D. APPLICANT: Willats, W. G. TITLE OF INVENTION: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -09-260-527-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                               33 AAQPAMAEVQLVQSGGGVERPGGSLRLSCAASGETEDDYGMSWVRQAPGKGLEWVSGI--
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                                                                                                                                                                           HVVFGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 309
                                                                                                                                                                                                                 QQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN
                                                                                                                                                                                                                                                                        EQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                70.7%; Score 1155; DB 3; 82.9%; Pred. No. 3.8e-83;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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; OTHER INFORMATION: Anti-homogalacturonan specific antibodies selected; OTHER INFORMATION: from a naive phage display library known as the COTHER INFORMATION: Synthetic scFv Library (#1) from the Centre for COTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge, UK US-09-260-527-3
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                                                                                                   PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR APPLICATION NUMBER: 60/327,367
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-06-04
PRIOR FILING DATE: 2001-06-04
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Best Local S
Matches 204
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CURRENT APPLICATION NUMBER: US/09/260,
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 53, Application US/10039785 Patent No. 6538938
SÓFTWARE:
SEQ ID NO 5
                                        PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL TITLE OF INVENTION: Receptors FILE REFERENCE: PF550
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Salcedo et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 AAQPAMAQVQLQESGPGLVKPSDTLSLTCAVSGYSISSSNWWGWIRQPPGKGLEWI-GYI 74
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73.4%;
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Pred. No. 8.6e
21; Mismatches
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8.6e-72;
hes 37;
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US-09-184-658-40
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Matches
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 40
LENGTH: 284
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                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measurement of Protein
TITLE OF INVENTION: Biological Media
FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Otterness,
                                         NAME/KEY: DOMAIN
LOCATION: (138)..(152)
THEORMATION: 15
                                                                                                     NAME/KEY: DOMAIN
LOCATION: (23)..(137)
OTHER INFORMATION: 9A4 VH
                                                                                                                                                                 LOCATION: (1)..(22)
OTHER INFORMATION:
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
NAME/KEY: DOMAIN LOCATION: (153)..(258)
                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                            OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
                               FEATURE:
                                                                                                                                                                                                              NAME/KEY: SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GQSPVLVIYQDNKRPSGIPERFSGSNSGNTATLKISGTQAMDEADYYCLAWDSSADW-VF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VTVSSGGGGSGGGGGGGAQSVLTQPPSVSVSPGQAARITCSGDKLGDKYASWYQQRP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.6%; Score 923.5; DB 4 ilarity 73.2%; Pred. No. 4.5e-65; Conservative 25; Mismatches 35
                                                                                                                                                                                              (22)
                                                                                                                                                                pCANTAB6 signal peptide; Val at likely the initiator Met.
                                                                                                                                                                                                                                            Description of Artificial Sequence: 9A4 scFv _{\rm VL}.
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                                            acid linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
US-09-184-658-63
                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 63
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 63,
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measure TITLE OF INVENTION: Biological Media FILE REFERENCE: PC9946-A
                                                                                                          NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: POOTHER INFORMATION: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Otterness, Iv
APPLICANT: Mezes, Peter
NAME/KEY:
LOCATION:
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LOCATION: (262)..(267)
OTHER INFORMATION: His
                                                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: scfv.
                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
                                            LOCATION: (23)..(138)
OTHER INFORMATION: 5109
                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                        TYPE: PRT
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                                                                            NAME/KEY: DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              234 AATYYCQQWRSYTR--TFGGGTKLEII-AAAHHHHHHGAAEQKLISEEDLNGAA 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  al Similarity 59.2
174; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09184658
                                                                                                          pCANTAB6 signal peptide;
likely initiator Met.
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er S.
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Best Local Similarity
Matches 180; Conserv
                                                                                                                                                          APPLICANT: YAMAMOTO, HIROKO
APPLICANT: YAMAMOTO, HAROKI
TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS B VIRU
TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC AGENT
TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
FILE REFERENCE: 0020-4882p
CURRENT APPLICATION UNMBER: US/09/486,814A
CURRENT APPLICATION UNMBER: US/09/486,814A
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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              FEATURE:
NAME/KEY:
LOCATION:
                                                                                                            LENGTH: 297
TYPE: PRT
ORGANISM: Mus sp.,
                                                   NAME/KEY: PEPTIDE LOCATION: (1)..(145)
OTHER INFORMATION: Identification Method:
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ION: (177)..(279)
INFORMATION: Identification Method:
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                             PEPTIDE
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YAMAMOTO, Hiroko
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SEQ ID NO 53
LENGTH: 334
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Matches
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Patent No. 6562347
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                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN F
FILE REFERENCE: 14014.0316/p
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR APPLICATION NUMBER: 60/077,745
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 19
                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
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266 SSGNHVVFGGGTKLTVLGAAAHHHHHH
                                                                                                                                                                                                           168;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAASGFTFDDYGMSWYRQAPGKGLEWYSGINWNGGSTGYADSYKGRYTISRDNAKNSLYL
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                                                                                                                                                                                                                                                                                     Similarity
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                                                                                                         GTTVTVSS-GGGGGGGGGGGGGS---SELTQDPAVSVALGQTVRITCQGDSLR---SYY
                               VNWYQKFPETAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYYCQCND
                                                           ASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRD
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                                                                                         FastSEQ for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QSPTTMAASPGEKITITCSASSSISSNYLHWYQQKPGFSPKLLIYRTSNLASGIPARFSG
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3: 57
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Pred. No. 2.8e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Version
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                                                                                                                                                                                                                                                                                                  Length 334;
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DSLSGWLFGGGTKLTVL---RHHHHHH 334

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RESULT 12
US-09-646-028-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Description of artificial sequence:/note-synthetic construct us-09-646-028-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUS:
                                          SOFTWARE: Fa
SEQ ID NO 51
LENGTH: 348
                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Kwak, Larry
APPLICANT: Biradyn, Arya
APPLICANT: Biradyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUS:
                                                                                                                                                                                                                                                                                Sequence 51, Appli Patent No. 6562347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
SEQ ID NO 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                       FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
                                                                                          PRIOR APPLICATION NUMBER: 60/PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR FILING DATE: 1
FEATURE:
           ORGANISM: Artificial Sequence
                              TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH: 339
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                                                                                                                                                                                                                                                                                                                                                                                                   266 SSGNHVVFGGGTKLTVLGAAAHHHHHH 292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          138 SGDTTYYADSVKGRFSASRDNSKNTYYLQMNNLRPNDTAVYFCAN--NQTGNFCLDNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                               256 VNWYQKFPETAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYYCQCND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTVTVSS-GGGGSGGGGGGGS---SELTQDPAVSVALGQTVRITCQGDSLR---SYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AQAPKSLEVQLLESGGGLVQSGGSLRLSCVASGLTFSSSAITWVRQAPGKGLEWVSGISF
                                                                                                                                                                                                                                                                                              Application US/09646028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.7%; Score 811; 61.0%; Pred. No. 4
                                                                                                                             60/077,745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            811; DB 4;
No. 4.1e-56;
                                                                                                                                                                                              FUSION PROTEINS AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64;
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; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct US-09-646-028-51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application Patent No. 6159947 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                   INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR TOWNTON NUMBER: WO PCT/FR94/00714
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                      APPLICATION NUMBER: WO PUBLICATION APPLICATION DATA:
APPLICATION NUMBER: FR 9:
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,164
                                                                                                                                                                                    FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Rhone-Poulenc
                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC
OPERATING SYSTEM:
TOPOLOGY:
                                                                                                TELEPHONE:
                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                      NAME: Savitzky, Martin F. REGISTRATION NUMBER: 29,6
                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Collegeville
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                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           154 ADSVKGRFSASRDNSKNTVYLQMNNLRPNDTAVYFCAN--NQTGNFCLDNWGQGTLVTVS
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              amino
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S-GGGGSGGGGSGGGS---SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQK 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVQLLESGGGLVQSGGSLRLSCVASGLTFSSSATTWVRQAPGKGLEWVSGISFSGDTTYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FGGGTKLTVL---RHHHHHH 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PETAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYYCQCNDDSLSGWL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500 Arcola Road,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tocque, Bruno
                                                                                  (610)454-3808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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                 acid
                                 amino acids
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                                                                                                                                                      29,699
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; Pred. No. 1.3e-55;
28; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rorer Inc.
3C43
                                                                                                                                       ST93030-US
                                                                                                                                                                                                                                                                                                                                                                                  Version #1.30
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APPLICANT: Carter, Paul J.

APPLICANT: Fendly, Brian M.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979

CURRENT APPLICATION NUMBER: US/08/918,148A

CURRENT FILING DATE: 1997-08-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 75

LENGTH: 245
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; ORGANISM: artificial
US-08-918-148-75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                              Query Match 48.1%; Score 785.5; DB 4; Best Local Similarity 64.0%; Pred. No. 2.8e-54; Matches 160; Conservative 29; Mismatches 54;
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                                                                                                    118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VVFGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLN 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH 270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTTVTVSSGGGGSGGGGSGGGSS-ELTQDP-AVSVALGQTVRITCQGDSLRSYYASWYQ
                                                                                                                                                       YYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARWSGEDA---FDIWGQGTMVT
                                                                                                                                                                                                            MAEVQLVQSGGGLVKPGGSLRLSCAASGFTFSDYYMSWIRQAPGKGLEWVSYISSSGSTI 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTTVTVSSGGGGSGGGGGGGGGDVELTQSPHSLSASLGETVSIECLASEGISNYLAWYQ
                       GTKLTVLGAA 285
                                                                                                    VSSGGGGSGGGGGGGDIVMTQSPSTLSASVGDRVAITCRASEGIYHWLAWYQQKPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TFGAGTKLEIKRA-----AAEQKLISEEDLN 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QKPGKSPQLLIYYASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYYCQQAYKYPS-
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                                                                                                                                                                                                                                                                54; Indels
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                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                          245;
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US-08-918-148-76
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APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
CURRENT APPLICATION NUMBER: US/08/918,148A
CURRENT FILING DATE: 1997-08-25
NUMBER OF SEQ ID NOS: 79
SEQ ID NO 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 76, Application US/08918148A Patent No. 6342220 GENERAL INFORMATION:
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Best Local
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APPLICANT: W.
APPLICANT: Carter, Paul J.
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time : 19.2546 secs
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## ALIGNMENTS

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Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer; tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR; TNF cytokine.
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WPI; 1999-045228/04.
N-PSDB; AAV72532.
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15-MAY-1997;
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                                                        caspase; apoptosis;
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                                                                                                                                                                                                        29-MAY-2002
                                                                                                                                                                                                                                                                                                                      ABB09603 standard; Protein;
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                                                                                                                                      acid sequence of single-chain Apo-2 antibody 16E2
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                                                                                   Apo-2; tumour necrosis factor receptor;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2. binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New nucleic acids encoding an Apo-2 ligand, useful for activating stimulating apoptosis in cancer cells, thus especially useful in treatment of cancer, or in enhancing immune-mediated cell death
                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 14; Fig 16; 68pp; English.
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N-PSDB; ABL41733.
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09-FEB-1998;
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                                                                       GNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAAEQKLI
                                                                                                             DPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSS
                                                                                                                            DPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSS
                                                                                                                                                                                   QMNSLRAEDTAVYYCAKILGAGRGWYFDLWGKGTTVTVSSGGGGSGGGGGGGGGGGSELTQ
                                                       GNTASLTITGAQA.EDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAAEQKLI
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SEEDLNGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence represents a single-chain Apo-2 antibody, desistantic from a phage library. It is believed that
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98US-074119P
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                                                                                                                                                                                                                                                                                                                                       Score 1633; DB 23; Pred. No. 7.9e-101; Mismatches 0;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Apo-2 apoptosis
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09-FEB-1998;
14-MAY-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, quantitative diagnostic assays, or in generating antibodies aga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 14; Fig 16; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB;
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apoptosis; tissue-specific typing; affinity purification;
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                                    GNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHHGAAEQKLI
                                                                                      DPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSS
                                                                                                                                                                                            CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL
SEEDLNGAA
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llarity 100.0%;
Conservative
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98US-0079029.
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Pred. No. 7.9e-101;
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                                                                                                                                                                     Human Apo-2 polypeptide inducing apoptosis conditions linked with decreased apoptosis e. antibodies to increase or decrease apoptosis
                                                                                                                                             The present invention describes human Apo-2. Apo-2 can be used
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15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                              Single chain
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                                                                                                                                                                                                                                                                                                                            cumour necrosis
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                                                                                                                                                                                                                                                                                                                     cytokine
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DB; AAV72533.
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                                                                                                                                                                                                                                                                                                                            receptor;
is factor;
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97US-0857216.
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                                                                                                                                                                                                                                                                                                                           apoptosis; neurodegenerative disease;
TNF; tumour necrosis factor receptor;
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                                                                                                                                                                             9.
                                                                                                                                                                                   useful to treat
                                                                                                                                                                             cancer,
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CC therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. CC App-2 is believed to be a new tumour necrosis factor (TNF) receptor CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by CC binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It CC can be used to identify agents activating Apo-2, useful to treat CC mammalian cancer cells, and to produce Apo-2 chimeras useful to therapeutically (e.g. those containing immunoglobulin sequences can be (inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined CC with a (particularly pharmaceutically acceptable) carrier in compositions CC comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block cercessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 cercessive apoptosis and antagonistic antibodies (e.g. to detect Apo-2 cercessive apoptosis and antagonistic antibodies (e.g. to detect Apo-2 cercessive apoptosis and apoptosis (e.g. to detect Apo-2 cercessive apoptosis and apoptosis (e.g. to detect Apo-2 cercessive apoptosis (e.g. to detect Apo-2 cercessive apoptosis (e.g. to detect Apo-2 cerces (e.g. to detect Apo-2 ce Sequence 312 AA;

Query Match Best Local S Matches 282 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS Conservative 89.4%; 8 Score 1460.5; Pred. No. 2.2e 8; Mismatches .2e-89; es 18; 5 Gaps 60

Similarity

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RESULT 5
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                                     20E6, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cance to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and i
                                                                                                                                                                            New nucleic acids encoding an Apo-2 ligand, stimulating apoptosis in cancer cells, thus treatment of cancer, or in enhancing immune.
                            affinity
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                   caspase;
                                                                                                                                                                                                                                                                                                                                                                                                                            Human; Apo-2; tumour necrosis factor receptor; TNFR; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB09604 standard;
                                                                                                                                                                                                                                                       Ashkenazi AJ
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                             purification
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                                                                                                                                     sequence
                                                                                                                                                                         acids encoding an Apo-2 ligand, useful for activating apoptosis in cancer cells, thus especially useful in t cancer, or in enhancing immune-mediated cell death.
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                                                                                                                          represents a single-chain Apo-2 antibody, des
                            of Apo-2
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                                                                                                                                                         English.
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                             recombinant cell culture or
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                                                           cancer,
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Sequence

312

A

The invention describes a novel isolated Apo-2 polypeptide. The *l* polypeptide is useful for inducing apoptosis in mammalian cells, or ex vivo gene therapy, in quantitative diagnostic assays, as a against samples containing unknown quantities of Apo-2, in genera

control

vivo

Example

Fig 16;

64pp; English

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RESULT 6
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09-FEB-1998;
14-MAY-1998;
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N-PSDB; ABX16408.
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tissue-specific typing; affinity
e-type receptor binding assay; mou
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                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal plattelet function; sulphated tyrosine-dependent protein-protein interaction.
  Novel
                                                                                 Lazarovits
Szanthon E,
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29-DEC-2000;
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Richter T,
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and
                                                                                 Nimrod A,
Peretz T,
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important
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                                                                                 Mar-Haim
Levanon
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cc inflammation, where the epitope is capable of being bound by an antibody.

Cc its antigen-binding fragment or its complex comprising at least one capable of the compression of the c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             important in inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tion relates to an isolated epitope present on ca
in physiological phenomena such as cell rolling,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cells and
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Query Match Best Local Sequence Similarity of the invention. 277 A, 78.4%; Score 1279.5; pred. No. 2e-7 4; Mismatches 2e-77; DB 23; Length 277;

infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody

Matches 213 250 273 190 130 153 93 16 251; 76 33 FGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 309 PGQAPYLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV GTTVTVSSGGGGSGGGSGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK NGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK 152 GTLVTVSRGGGGSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK NGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLTHP----YF--WGQ FGGGTKLTVLGA----PGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV Conservative 4; -AAEQKLISEEDLNGAA 7; Indels 15; Gaps 212 129 272 189 75 249

ABG78328 standard; Protein; 밁 Q В QΥ 밁 δÃ Ър Š Вþ

ABG78328;

15-NOV-2002

(first entry)

Human Fv molecule hypervariable region related peptide

Human; Fv disulfide Homo sapiens. lymphoma; molecule; hypervariable region; single chain Fv; cytostatic; Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adeno myeloma; blastoma; seminoma; melanoma; acute myeloid leukaem leukaemia; e myeloid le

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Best Local S
Matches 251
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Plaksin I
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  Human
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                                                                              ABG91841 standard;
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)B; ,ABS63384.
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antibody
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                                                                                                                                                                                                                                                   NGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK 152
                                                                                                                                                                                                                                                                                                                                                                          AAQPAMAEVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
                                                                                                                                                             FGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 309
                                                                                                                                                                                                                                                                                                        NGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARLTHP----YF--WGQ
                                                                                                                                                                                                                                                                                                                                                           AAQPAMAEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            invention.
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t of fragment with enhanced binding
selectively bind target cell in favour of other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Guy R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English
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Pred. No. 2e-77;
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60 A B

PGQAPVLVIYGKNINRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVV

GTTVTVSSGGGGSGGGGSGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQK

212

189 272 NGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRAP-----VIWGQ

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                                                                                                                                                                                                                                                                                                         The invention relates to an isolated epitope present on cancer cells and C important in physiological phenomena such as cell rolling, metastasis and c inflammation, where the epitope is capable of being bound by an antibody, cris antigen-binding fragment or its complex comprising at least one antibody or its binding fragment having a first hypervariable region. The C epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC disease, thrombosis, restenosis, metastasis, growth and/or replication of C tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, for increasing mortality of tumour or leukaemia cells, for increasing the cusceptibility of diseased cells to damage by anti-disease, anti-cancer cor anti-leukaemia agents, or for decreasing the number of tumour or the above mentioned purposes. The epitopes are useful for diagnosing and treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial cor inflammatory diseases, cardiovascular diseases such as myocardial platelet function and diseases caused by sulphated tyrosine-dependent protein protein interactions. This sequence represents a human antibody
                                                                                                                                                                                             Query Match
Best Local S
Matches 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or carding inflammation, the contract of the con
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29-DEC-2000;
                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                          Similarity
NGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK
                                                                                                     AAQPAMAEVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
                                                                                    AAQPAMAEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Page 233-234; 310pp; English
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                                                                                                                                                                                                Conservative
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Richter T,
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2000US-0751181.
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                                                                                                                                                                                                                                                                                                                                                                invention.
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Amit B, Kooperman
                                                                                                                                                                                       Score 1275.5; DB 23
Pred. No. 3.7e-77;
Mismatches 8;
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operman L,
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abnormal platelet function;
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Levanon
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                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of other
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                    myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is accute myeloid leukaemia cell). The peptide is also useful for preparing composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region related peptide of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adeno
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG78150 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-DEC-2000;
                                                                                                                                                                                                   Local
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                                                                              AAQPAMAEVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
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  NGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK 152
                                                    AAQPAMAEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
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Peretz T;
                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0751181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           blastoma; seminoma; melanoma; acute myeloid leukaemia.
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89.9%;
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                      the present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by CC binding to TNFs, and Apo-2 triggered caspase-dependent apoptosis. It CC can be used to identify agents activating Apo-2, useful to treat CC mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be contained to produce Apo-2 or inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined CC with a (particularly pharmaceutically acceptable) carrier in compositions CC comprising first and second Apo-2 antibodies). Agonistic (especially csingle-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block cseciesive apoptosis (e.g. in neurodegenerative diseases). Apo-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and antibodies to increase or decrease apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 14; Fig 16; 134pp; English.
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15-MAY-1997;
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   apoptosis (e.g. in
may also be used
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97US-0857216
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   in neurodegenerative diseases). ed diagnostically e.g. to detect
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                                                                                                   New nucleic acids encoding an Apo-2 ligand, stimulating apoptosis in cancer cells, thus treatment of cancer, or in enhancing immune.
  The present 24C4, which
                                                            Example 14; Fig 16; 68pp; English
                                                                                                                                                                                         N-PSDB;
                                                                                                                                                                                                                                                                                                                                     15-MAY-1997;
09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; Apo-2;
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                                                                                                                                                                                                                                                     Ashkenazi AJ
                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                 14-MAY-1998;
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DB; ABL41735.
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sequence represents a single-chain is isolated from a phage library. ]
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                                                                                                                                                                                                                                                                                                                                     97US-046615P.
98US-074119P.
                                                                                                                                                                                                                                                                                                                                                                                                 98US-0079029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
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78.0%;
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red. No. 3.5e
Mismatches
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                                                                                                   ligand, useful for activating s, thus especially useful in immune-mediated cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .5e-74;
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n Apo-2 .
It is b
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  2 antibody, designated
believed that
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Best Local Similarity
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09-FEB-1998;
14-MAY-1998;
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                                                                                                                                                                                                                    Apo-2; tumour necrosis factor family; TNFR; apoptosis; tissue-specific typing; affinity competitive-type receptor binding assay; mou
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                                               (GETH ) GENENTECH INC
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                                                                                                                                                                                                                                                                       antibody
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98US-074119P.
98US-0079029.
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                                                                                                                                                                                                                                                                                                                                             Protein;
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78.0%;
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                                                                                                                                                                                                                                                                     fragment 24C4.
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Matches 245
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                                                                                                                                                                   Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet functisulphated tyrosine-dependent protein-protein interaction.
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                                                                           WO200253700-A2
                                                                                                                                                                                                                                                                                                                   Human antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                ₿
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RESULT 1: ABP46027

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                                                                                                                                                                                                                                                                           The invention relates to an isolated epitope present on cancer cells and CC important in physiological phenomena such as cell rolling, metastasis and CC inflammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC epitopes are useful for increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia CC etlls in a patient, cell-cell, cell-matrix, platelet-matrix, platelet-platelet adhesion or aggregation, for CC increasing mortality of tumour or leukaemia cells, for increasing the susceptibility of diseased cells to damage by anti-disease, anti-cancer CC or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diagnosing and CC treating diseases such as cancer, leukaemia, autoimmune diseases,
                                                                                                                                                                                                        Best | Local
Matches 2
                                                                                                                                                                                                                                        Query Match
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Szanthon E,
                                                                                                                                                                                                                                                                                                                                           inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abno platelet function and diseases caused by sulphated tyrosine-dependent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        physiological phenominflammation, for tradiseases, and cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel isolated epitope present on cancer cells and importions physiological phenomena such as cell rolling, metastasis inflammation, for treating autoimmune, inflammatory or co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                29-DEC-2000;
29-DEC-2000;
                                                                                                                                                                                                                                                                                                           protein-protein interactions. This sequence represents \mathbf{f}_{r}^{\star}\mathbf{a}\mathsf{g}\mathsf{ment} of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                           Sequence
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AAQPAMAEVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
                                                                                   NGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK 152
                                                                                                                                      AAQPAMAEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
                                                                     NGGSTGYADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARMRAP-----VIWGQ
                                                                                                                                                                                                                                                                           266
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                                                                                                                                                                                                         Conservative
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2000US-0751181.
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Richter T,
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Pred. No. 1.1e
5; Mismatches
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                                                                                                                                                                                                                                                                                                                             human antibody
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                                                                                                                                                                                                                                                                                            This invention describes novel antibodies that immunospecifically bind to CC B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the CC tumour necrosis factor (TME) super family and induces B cell CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory. CC entirheumatic and antiAIDs activity and can be used in vaccines to CC inhibit the expression and activity and can be used in vaccines to CC and so may be used to detect and quantitate the presence of BLyS in CC and so may be used to detect and quantitate the presence of BLyS in CC indicated with aberrant expression of BLyS. They may also be associated with aberrant expression of BLyS. They may also be CC administered to treat diseases associated with aberrant and autoimmune disorders and CC administered to treat diseases associated with aberrant blyS expression CC and activity such as cancer, immune, and autoimmune disorders and CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and CC acquired immunodeficiency syndrome (AIDS)). ABP47228 represent to the arthrodies and frammonts of the arthrodies after the arthrodies are the arthrodies and the present contains and authorities are appresent contained and activate and arthrodies and arthrodies and arthrodies and arthrodies and arthrodies are appresent.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-JUN-2000; 2000US-212210P.
17-CCT-2000; 2000US-240B1BP.
16-MAR-2001; 2001US-276248P.
21-MAR-2001; 2001US-277379P.
25-MAY-2001; 2001US-293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-114799/15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           common variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-JAN-2002.
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                                                                                                                                                                                                                                                                                                                                              antibodies and
     116
                                       160
                                                                    228;
                                                                                                                                                             40 EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
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                                                                                                                                                                                                                                                                                                                             invention.
                                                                                                                                                                                                                                      Similarity
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CAMBRIDGE ANTIBODY TECHNOLOGY.
EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
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                                                                                                                                                                                                                                                                                                                                            fragments of the antibodies described in the method
                                                                                                                                                                                                                                    73.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3148pp; English.
                                                                                                                                                                                                                Score 1194.5; DB 23
Pred. No. 7.6e-72;
""matches 7;
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Search completed: September 22, 2003, 15:18:43 Job time: 52.7766 secs

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Result
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Listing first 45 summaries
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Perfect score:
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Match
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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US-09-880-748-2038

US-09-880-748-2013

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US-09-880-748-2013

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US-10-288-917-9
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9-880-748-194	-09-880-748-2	9-880-748-203	-09-880-748-9	9-880-748-9	-09-880-748-194	-09-880-748-1	0-748-197	-09-880-748-9	-09-880-748-9	-09-880-748-176	-09-880-748-1	-880-748-110	9-880-748-9	-09-880-748-1	-09-880-748-9	-09-880-748-2	-09-880-748-174	-09-880-748-9	-09-880-748-2	-09-880-748-191	-09-880-748-9	-09-880-748-	0-748-1	-09-880-748-201	-09-880-748-9	-09-880-748-9	-880-748-202	S-09-880-748-1	9-039-7	
194	∾	2039,	913,	924,	1942,	Ü		•	908,	Sequence 1764, Ap	1826,	110	996,	Sequence 1929, Ap	952,	Sequence 2035, Ap	1740,	963,	çı	191	914,	e 835,	e 1335,	e 2018,	e 920,	e 916, A	equence 2022,	equence 1323,	Αp	

## ALIGNMENTS

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Sequence 9, Application US/10288917

Sequence 9, Application US/10288917

Publication No. US20030148455A1

GENERAL INFORMATION:

APPLICANT: Adams, Camilia W.
APPLICANT: Adams, Camilia W.
APPLICANT: Adams, Apo-2

Chuntharapai, Anan

Chuntharapai, Anan

TITLE OF INVENTION: Apo-2 Receptor

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USAN

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinDatin (Genentech)

CURRENT APPLICATION NUMBER: US/10/288,917

FILING DATE: 06-No. US20030148455A1-2002

CLASSIFICATION NUMBER: 10/052798

FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029

FILING DATE: 14-MAY-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 15-MAY-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 15-MAY-1997

ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
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309; 0;

Gaps

0

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RESULT 2
US-10-052-798-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/10052798 Publication No. US20020150985A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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Best Local Similarity
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILLING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14 CORRESPONDENCE ADDRESS: ADDRESSE: Genentech, Inc.
                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                     CITY: South San F
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEEDLNGAA 309
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Kim, Kyung J.
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                                                                                                                                                                                                                                                                                      Francisco
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BER: P1101R2D1C1
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US-10-288-917-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 10, Application US/10288917 Publication No. US20030148455A1 GENERAL INFORMATION:
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Best Local Similarity
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                             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-No. US20030148455A1-2002
CLASSIFICATION: CUMPATA:
PRICE TOTAL NUMBER: 10.065770
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Apo-2 Receptor
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APPLICATION NUMBER: 10/052798 FILING DATE: 02-NOV-2001
                                                                                                                                                                                                                                                     CITY: South San F
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEEDLNGAA 309
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                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                        STREET: 1 DNA Way
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REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 309 amino acids
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Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                                                                      Sequence 10, Ap
Publication No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/046615
FILING DATE: 15-KAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                       APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: South San F. STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
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TELEFAX: 650/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 09/079029 FILING DATE: 14-MAY-1998
                                                                                                      COUNTRY: USA
                                                                                                                                                       STREET:
                                                                                                                                                                      ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH:
                                                                                                                                                                                                                                                                                                                                        Application US/10052798
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                                                                                                                                                                                                                                                      Chuntharapai, Anan
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90.1%;
                                                                                                                                     Francisco
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US-10-288-917-11
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                                                                                                                                                                                                                                                                                  Sequence 11, Application No. US2003 GENERAL INFORMATION:
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ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/079,029
FILING DATE: <UNKNOWN>
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/052,798
FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                               Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
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                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                    APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QMNSLRAEDTAVYYCA----KILGAGRGWYFDLWGKGTTVTVSSGGGGGGGGGGGGGGGSS
                                                                                                  CITY: South San Fi
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                        QKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHHGAAE
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TOPOLOGY: Linear
                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 312 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
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                                                                                                                                     STREET: 1 DNA Way
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                                                                                     USA
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90.1%;
                                                                                                                    Francisco
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                                                                                                                                                   Inc.
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299 296 239 179

236

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Gaps

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RESULT 6
US-10-052-798-11
(S-quence 11, Application US/10052798
; Publication No. US20020150985A1
; Publication No. US20020150985A1
; GENERAL INFORMATION:
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Best Local Sim
Matches 245;
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APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
    CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA WAY
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-No. US20030148455A1-2002
CLASSIFICATION: CUNKNOWN>
                                                                                  Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                       APPLICANT: Adams, Camilia W.
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                                                                                                                                                                                                                                                                                                                                                          EQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                           EQKLISEEDLNGAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                      SGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHHGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAA 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPPSVSGAPGORVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QMNSLRAEDTAVYYCAR----DRGYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGGGSQSVL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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                                                                                                                                             Ashkenazi, Avi J.
Chuntharapai, Anan
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78.0%;
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Best Local Similarity
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APPLICANT: Ruben et al.
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: 11: SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US/09/079,029
FILING DATE: <UNknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 1
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                                                                                                                                                                                                                                                                                                                                   EQKLISEEDLNGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/10/052,798 FILING DATE: 02-No. US20020150985A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: P1101R2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 310 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.4%; Score 1231.5; DB 14; Length 310; 78.0%; Pred. No. 1.7e-79;
                                                                                                                                                                                                                                                                                                                                   310
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Indels

9: Gaps

Bind

295

296

235 176

236

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PRIOR APPLICATION NUMBER: 0.21
PRIOR FILING DATE: 2001-03-25
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2038
LENGTH: 239
TYPE: PRT
                                                                                                                                        NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 937
LENGTH: 239
TYPE: no.
                 S
                                                                                                        ; TYPE: PRT
; ORGANISM: HOMO
US-09-880-748-937
                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-09-880-748-937
: Sequence 937, Application US/09880748
: Publication No. US20030059937A1
: GENERAL INFORMATION:
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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                                          Query Match
Best Local Similarity
Matches 227; Conserv
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Best Local Similarity
Matches 228; Conserv
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ruben et al. TITLE OF INVENTION: Ant FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/276,248 FILING DATE: 2001-03-16
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                                              72.8%; ilarity 93.0%; Conservative
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                                                                                                                        sapiens
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93.48;
                                           Score 1189.5; DB 11; Length Pred. No. 1.2e-76; 4; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1194.5; DB 11
Pred. No. 5.4e-77;
4; Mismatches 7;
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                                             Gaps
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                 99
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	236 TVLC 239	를 -
	280 TVLG 283	φ 
235		문 4
370		₽ —-
175		<b>В</b>
219	160 SGGGGSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVL	Q 
159 115	100 ADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGKGTTVTVS 	
60	40 EVQLVQSGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY	B 8
۲	Query Match 72.2%; Score 1178.5; DB 11; Length 239; Best Local Similarity 91.8%; Pred. No. 7.3e-76; Matches 224; Conservative 7; Mismatches 8; Indels 5; Gaps	Que Bes Mat
	0-880-748-2015	US-09
	HOMO sani	 o_⊢a ı
	ID NO 2015 ENGTH: 239	SEQ
	NUMBER OF SEQ ID NOS: 3239 SOFTWARE: Patentin Ver. 2.0	SO
	IOR FILING DATE: 200	PR
	IOR FILING DATE: 2001-03-21	P 7
	FILING DATE: 2001-03-16	 B.B.
	PRIOR APPLICATION NUMBER: 60/276,248	 P. X
	APPLICATION N	PR.
	PRIOR FILING DATE: 2000-06-15	 P. X
	FILING DATE: 2001-06-15	20
	REFERENCE: PF523 NT APPLICATION NUMBER: US/09/880,748	C FI
	INVENTION:	H.
		GEN
	SULT 9 -09-880-748-2015 Sequence 2015, Application US/09880748 Publication No. US20030059937A1	RESULT US-09-
	236 TVLG 239	Db
	280 TVLG 283	у у
235	176 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKL	Db
279	220 VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKL	Ωγ
175	116 RGGGSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVL	Вb
219		Qy
115	61 ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARRRYALDYWGQGTLVTVS	당
159	RVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGK	ογ
60	1 EVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY	Db

RESULT 10

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RESULT 11
US-09-880-748-1416
; Sequence 1416, Application US/09880748
; Sequence 100 No. US20030059937A1
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
PRIOR FILING DATE: 2001-05-25
NUMBER: BATGATA VAR
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                                                        PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
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SEQ ID NO 2013
. LENGTH: 240
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CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 218; Conserva
APPLICATION NUMBER: 60/293,499
FILING DATE: 2001-05-25
R OF SEQ ID NOS: 3239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKL 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SGGGGSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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APPLICANT: BASU, AMARCSH
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRA
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRA
TITLE OF INVENTION: ACENTS ACROSS CELLULAR BARRIERS
FILE REFERENCE: 057220-0303
CURRENT APPLICATION NUMBER: US.60/969,748C
CURRENT FILING DATE: 2000-12-0
PRIOR APPLICATION NUMBER: US.60/267,601
PRIOR APPLICATION NUMBER: US.60/248,819
PRIOR FILING DATE: 2000-11-14
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US.60/248,478
PRIOR APPLICATION NUMBER: US.60/248,478
PRIOR APPLICATION NUMBER: US.60/237,929
PRIOR FILING DATE: 2000-11-13
PRIOR APPLICATION NUMBER: US.60/237,929
PRIOR FILING DATE: 2000-10-02
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US-09-969-748C-2
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS,
APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHERIDAN, Philip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYAN, Jacqueline, M.
APPLICANT: CHAPIN, Steven
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn
SEQ ID NO 1416
LENGTH: 252
                                                                                                                                                                                                                         SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09969748C Publication No. US20030161809A1
                                                                         Matches
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                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 115
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                    LENGTH: 2
TYPE: PRT
                                                                                                                                                               ORGANISM: Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 QRTMVTVSSGGGGSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQ
                 33 AAQPAMA-----EVQLVQSGGGVERPGGSLRLSCAASGFTEDDYGMSWVRQAPGKGLEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 ADSVKGRETISRDNAKNSLYLQMNSLRAEDTALYYCAKDRGVGYDILTGRTYYYGMDVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                                                                      290
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                                                                                        Similarity
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AAQPAMADYKAKQVQLVQSGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKGLEWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VFGGGTKLTVLG
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                                                                         Conservative
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                                                                                      69.1%;
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86.9%; Pred. No. 5.5e-73;
tive 11; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
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                                                                         18;
                                                                     Score 1129; DB 12;
Pred. No. 2.8e-72;
8; Mismatches 20;
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                                                                                                       Length 290;
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Sequence 2023, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: HAWLEY, STEPHEN B.

TITLE OF INVENTION: COMPOUNDS AND MOLECULAR COMPLEXES COMPRISING MULTIPLE
TITLE OF INVENTION: BINDING REGIONS DIRECTED TO TRANSCYTOTIC LIGANDS
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No. US20030166160A1 GENERAL INFORMATION:
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Best Local :
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TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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80.1%;
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Pred. No. 2.8e-72;
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PRIOR APPLICATION NUMBER: US 60/267,601
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: US 60/248,819
PRIOR FILING DATE: 2000-11-14
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/248,478
PRIOR APPLICATION NUMBER: US 60/237,929
PRIOR FILING DATE: 2000-11-13
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 115
SOFTWARE: PATENTIN VETSION 3.0
SEQ ID NO 12
LENGTH: 296
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PRIOR FILING DATE: 2000-06-15
PRIOR PRIOR PRICIN NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-25
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: ARIZEKE PHARMACEUTICALS,
APPLICANT: HOUSTON, Lou, L.
APPLICANT: SHERUDAN, Philip, J.
APPLICANT: HAWLEY, Stephen
APPLICANT: GLYNN, Jacqueline, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2023
LENGTH: 239
TYPE: PRT
                   SEQ
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Best Local :
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Pred. No. 6.5e
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACT TITLE OF INVENTION: ACENTS ACROSS CELLULAR BARRIERS FILE REFERENCE: 057220-0303 CURRENT APPLICATION NUMBER: US/09/969,748C CURRENT FILING DATE: 2002-12-10 CURRENT FILING DATE: 2002-12-10
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Search completed: September 22, 2003, 15:36:23 Job time : 35.1858 secs

Title: Perfect score: Sequence:

US-10-052-798-9 1633

Run

OM protein on:

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Scoring table:

BLOSUM62 Gapop 10.0 , 283308 seqs,

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Total number of hits satisfying chosen parameters:
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C; Species: Mus musculus (house mouse)
C; Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_chang
C; Accession: A56446
R; Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A; Title: A high affinity digoxin-binding protein displayed on A; Reference number: A56446; MUID:95229583; PMID:7713873
A; Accession: A56446
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-268 <TAN>
A; Cross references: GB:U20617
C; Keywords: heterotetramer; immunoglobulin
                  RESULT 2
$41374
$41374
$single chain FV antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_cha
C;Accession: $41374
R;Artsaenko, O; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization
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      number:
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RESULT 4
$47.184

Ig lambda chain - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change:
C; Accession: $47184
A; McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
submitted to the EMBL Data Library, June 1994
A; Description: Cloning and analysis of IgM anti-thyroglobulin au:
A; Reference number: $47181
A; Accession: $47184
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$19663

Ig lambda chain V region (clone alpha-BSA3) - human

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: $19663

R.Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.D.; McCafferty, J.; Griffiths, i

J.Mol. Biol. 222, 581-597, 1991
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A;Molecule type: mRNA
A;Residues: 1-109 <mAR>
A;Residues: 1-109 <mAR>
A;Cross-references: EMBL:X61640; NID:g29492; PIDN:CAA43821.1; PID:g1340166
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-89/Domain: immunoglobulin homology <IMM>
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A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-249 < ART>
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Pred. No. 3.8e-31;
8; Mismatches 73;
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A; Note: the nucleotide sequence was submitted to the EMBL Data Library, (C; Superfamily: immunoglobulin V region; immunoglobulin homology C; Keywords: heterotetramer; immunoglobulin homology F; 13-98/Domain: immunoglobulin homology

A;Status: preliminary; nucleic acid sequence not A;Molecule type: mRNA A;Residues: 1-121 <RAA>

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A; Accession: S31104

#text\_change 23-Jul-1999

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R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, EMBO J. 12, 725-734, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ig lambda chain V region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
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A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
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98.2%;
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RESULT 7

$70444

$70444

Ig lambda chain precursor V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change

C;Accession: $70444; $70426

R;Cuisinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.

Mol. Immunol. 29, 1363-1373, 1992

A;Title: IgM kappa/lambda EBV human B cell clone: an early step

A;Reference number: $70442; MUID:93024508; PMID:1383695
                                                                                                                                                  Ig lambda chain - human (fragment)
c;Species: Homo sapiens (man)
c;Species: Homo sapiens (man)
c;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #tex
C;Accession: S38498
C;Accession: S38498
C;Accession: By Ouwehland, W.H.; Bye, J.M.; Finnern, R.;
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for hu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:X53070
A;Experimental source: cell line E29.1, clone VL 29-1
C;Superfamily: immunoglobulin v region; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: h
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A;Residues: 1-127 <CUI>
A;Experimental source: clone
R;Tonnelle, C.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-108 <MAR>
                                                                                           A; Reference number: S38488
A; Accession: S38498
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A; Residues: 1-90 <TON>
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A;Status: not compared with conceptual translation
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Best Local
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1; Mis
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Pred. No. 9e-30;
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R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R. submitted to the EMBL Data Library, June 1993 A;Description: Human antibody fragments specific for
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C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S38496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:223035; NID:g414043; PIDN:CAA80570.1; PID:g414044 C;Superfamily: immunoglobulin V region; immunoglobulin homology C:Keywords: heterotetramer; immunoglobulin C:Keywords: heterotetramer; immunoglobulin F:14-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                           RESULT
JC5322
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                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically b:
                                                                                                                                                                                  Biochém. Biophys. Res. Commun. 230, 242-246, 1997
A;Title: Characterization of scFv-421, a single-chain antibody
A;Reference number: JC5322; MUID:97168950; PMID:9016757
A;Accession: JC5322
                                                                                                                                                                                                                                                                                     C;Species: Homo sapiens (man)
C;Daté: 15-May-1997 #sequence_revision 15-May-1997
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C;Superfamily: immunoglobulin V region; immunoglobulin homology
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A; Residues: 1-109 <MAR>
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                                                                                                                                                                                                                                     R; Jannot, C.B.; Hynes, N.E.
Biochem. Biophys. Res. Commun.
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Best Local S
Matches 117
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61 FSGSYPGNTASLTITGAQAEDEADYYCTSRDTSGNHVLFGGGTKLTVLG
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                                                                                                                  specifically binds the tumor suppressor protein
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93.6%;
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                                                  Score 531.5; DB 2;
Pred. No. 1.6e-28;
4; Mismatches 74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 539; DB 2;
Pred. No. 2.4e-29;
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Pred. No. 1
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.7e-29;
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ESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSSG

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Ig lambda chain V-III region (Sh) - human
C;Species: Homo sapiens (man)
C;Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 02-Sep-1997
C;Accession: A01980
R;Titani, K.; Wikler, M.; Shinoda, T.; Putnam, F.W.
J. Biol. Chem. 245, 2171-2176, 1970
A;Title: The amino acid sequence of a lambda type Bence-Jones protein. III. The A;Reference number: A92057; MUID:70166723; PMID:4909564
A;Accession: A01980
A;Accession: A01980
A;Accession: A01980
A;Residues: 1-108 <TIT>
A;Note: the sequence of the C region is also given
C;GenetLcs:
A;Gene: GDB::GLV@
A;Cross-references: GDB::119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical 1: hain disulfide bonds. In some cases, such as IgA and IgM, the subunits association: Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin homology
C;Keywords: interpretation: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Species: Homo sapiens (man)
C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Caccession: 825748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunola; Reference number: 816439; MUID:91257162; PMID:1904362
A;Accession: 825748
A;Accession: 825748
A;Status: prelininary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-233 <COM>
A;Cross-references: EMBL:857813; NID:933725; PIDN:CAA40950.1; PID:933726
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;148-216/Domain: immunoglobulin homology <IMM>
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L3HUSH
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                                                                                              An immunoglobulin heterotetramer subunit consists of two identical light (ka
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91.7%;
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Pred. No. 2e-28;
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Ig lambda chain V-IV region - human (tentative sequence) (fragments)
N; Alternate names: amyloid-fibril protein GIL
C; Species: Homo sapiens (man)
C; Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 31-1
C; Accession: S02083
R; Fykse, E.M.; Sletten, K.; Husby, G.; Cornwell III, G.G.
Biochem. J. 256, 973-980, 1988
A; Title: The primary structure of the variable region of an immunog.
A; Reference number: S02083; MUID:89134210; pMID:3146981
A; Accession: S02083
A; Molecule type: protein
A; Residues: 1-70;71-72;73-75;76-131;132-146 <FYK>
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F;14-88/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Title: By-passing immunization. Human antibodies from V-gene A;Reference number: S19663; MUID:92085276; PMID:1748994
A;Recession: S19672
A;Molecule type: mRNA
A;Residues: 1-110 <MAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig lambda chain V region (clone alpha-TEL14) - human C;Species: Homo sapiens (man) C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change C;Accession: S19672 R;Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; J. Mol. Biol. 222, 581-597, 1991
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                                                 SELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF
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91.8%;
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                                                                                                  Pred. No. 8.56
7; Mismatches
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Pred. No. 5.5e-28;
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Pred. No. 1.5e-28;
                                                                                                                                 Score
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No. 8.5e-28;
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                                                                                                                                                                                                                                                                                   immunoglobulin
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     282
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submitted to the EMBL Data Library, October 1992
A; Reference number: $30520
A; Accession: $30532
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-123 <MAR>
A; Residues: 1-123 <MAR>
A; Cross-references: EMBL:218318
C; Superfamily: immunoglobulin V region; immunoglobulin bomology
C; Keywords: heterotetramer; immunoglobulin
F; 15-98/Domain: immunoglobulin homology <IMM>
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30532
Ig heavy chain V region - human
C; Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Aug-1996
C;Accession: S30532
R;Mariette, X.
R;Mariette, X.
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Search completed: September 22, 2003, 15:14:58 Job time: 21.9098 secs
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                                                                                            158 VSS 160
                                                                                                                                       121 VSS 123
                                                                                                                                                                                                              61 SGSSSGNTASLTITGARAEDEADYYCNSRNSSGNYHVIFGGGTKLTVL 108
                                                                                                                                                                                                                                                                                                                    Length 123;
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Title: Perfect score: Sequence:

US-10-052-798-9 1633

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Copyright

GenCore version (c) 1993 - 2003

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Scoring table:

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RESULT 2
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LV3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                          AMEDLINE-70166723; PubMed-4909564;
A fitani K, Wikler M, Shinoda T, Putnam F.W.;
I'The amino acid sequence of a lambda type Bence-Jones protein. 3. 'I'The amino acid sequence and the location of the disulfide at philoges.";
J. Biol. Chem. 245:2171-2176(1970).
C. -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C. -!- MISCELLANEOUS: THIS IS A BENCE-JONES PROTEIN.
C. -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP: P80748; 2LOI.
DR GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005555; Pi.mmune response; NASS.
DR GO:00005555; Pi.mmune response; NASS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003506; Ig_MIC.
DR InterPro; IPR003506; Ig_MIC.
DR InterPro; IPR003506; Ig_MIC.
DR Ffam: PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROMAIN 1 97 IG-LIKE.
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DOMAIN 1
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NON_TER 108
SEQUENCE 108
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p01714;
p171714;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15 lambda chain V-III region SH.
19 lambda chain V-III region SH.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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HY3M_HUMAN
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HY41_MOUSE
HY31_MOUSE
LY4C_HUMAN
HY53_MOUSE
LY4C_HUMAN
HY53_MOUSE
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Pred. No. 2.4e
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Result No.

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Match Query

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Description

SUMMARIES

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HV19\_MOUSE HV19\_MOUSE HV3A\_HUMAN HV16\_MOUSE

P01714
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P01767
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HV3H\_HUMAN HV20\_MOUSE HV18\_MOUSE

HV01\_CANFA HV21\_MOUSE HV38\_MOUSE HV3I\_HUMAN HV3D\_HUMAN HV3B\_HUMAN HV3G\_HUMAN HV3U\_HUMAN HV3J\_HUMAN

HV22\_MOUSE HV05\_CARAU HV24\_MOUSE

HV3K\_HUMAN
HV3L\_HUMAN
HV3L\_HUMAN
HV25\_MOUSE
HV40\_MOUSE
HV57\_MOUSE
HV55\_MOUSE
HV55\_MOUSE

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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length: 0 length: 2000000000

Total number of hits satisfying chosen parameters:

127863

Searched:

127863 seqs,

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Database

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Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
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21-JUL-1986 (Re
15-SEP-2003 (Re
Ig heavy chain
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SEQUENCE
                                                                                                HV3F_HUMAN STANDARD; PRT; 1

P01767;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

15-SEP-2003 (Rel. 42, Last annotation

15 heavy chain V-III region BUT.
                                                                                                                                                                    HUMAN
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  MEDLINE-78137069; PubMed-416441;
Torano A., Putnam F.W.;
"Complete amino acid sequence of
                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (JUN-1975) to -i- MISCELLANEOUS: THIS
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Mammalia; Eutheria;
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Homo sapiens
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                                                                                        Homo sapiens (Human).
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G0:0005576; C:extracellular; NAS.
G0:0003823; F:antigen binding activity;
G0:0006955; P:immune response; NAS.
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Primates;
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Pred. No. 6.4e-25;
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                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region.
DOMAIN 1 111
                     EMBL; J00236; AAA53516
EMBL; M35415; AAA58735
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
                                                                                                                                                                                                                                                                                                               HV3C_HUMAN STANDARD; PRT; 1

P01764;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence up

15-SEP-2003 (Rel. 42, Last annotation
                                                                           use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                  Matthyssens G., Rabbitts T.H.; Structure and multiplicity of genes for the huma heavy chain variable region."; Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).-!- SIMILARITY: Contains 1 immunoglobulin-like dc
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NON_TER
                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=81101090; PubMed=6450418; Matthyssens G., Rabbitts T.H.;
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Eukaryota; Metazoa; Chordata;
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AAA58735.1;
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                                                                                                                                                                                                       immunoglobulin
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                                                                                                                           restrictions
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                                                                                                                                     collaboration -
                                                                                                    in no way commercial
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Genew;

GO:0005576;

HGNC:5545; IGHV@. :0005576; C:extracellular;

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160

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160

100

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120

159 60

QVKLVQAGGGVVQPGRSLRLSCIASGFTFSNYGMHWVRQAPGKGLEWVAVIWYNGSRTYY

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InterPro; IPROUSS...

R Pfam; PF00047; ig; 1.

R SMART; SM00406; IGy; 1.

DR PROSITE; PS50835; IG_LIKE; 1.

FT Immunoglobulin V region; Signal; 3D-structure.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V-I.

CHAIN 20 >117 IG-LIKE.

117 117 17582 MW; E826733F1A3CB0F
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                                                                                                                                                                   GO; GO:000302.,
GO:0006955; P:immune ....
GO; GO:0006955; P:immune ....
GO; GO:0006955; P:immune ....
GO; GO:0006955; P:immune ....
GO:0006955; P:immune ....
GO:0006955; P:immune ....
InterPro; IPR003706; Ig-v.
R Pfam: PF00047; 19; 1.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
JR PROSITE; PS50835; IG_LIKE; 1.
JR PROSITE; PS50835; IG_LIKE; 1.
JR Immunoglobulin V region; Pyrrolidone carboxylic acid.
Immunoglobulin V region; Pyrrolidone CARBOXYLIC ACITED ACITED
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Best Local S
Matches 81
                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-79124695; PubMed-420800; Chiu Y.-Y.H., Lopez de Castro J.A., Pc "Amino acid sequence of the VH region cryoimmunoglobulin IgG Hil."; Blochemistry 18:553-560(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region HIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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P01771;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activity; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A02054; G1HUHL.
; P01772; 2FB4.
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EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
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                                                                            Conservative
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                                                                                              26.2%;
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                                                                                                   Score 428;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 429;
Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E826733F1A3CB0F1 CRC64;
                                                                          Mismatches
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on of human
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2.6e-24;
nes 9;
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                                                                                                                   Length 121;
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Query Match
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Matches 84
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GO; GO:0005576; C:sattracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MEC.
InterPro; IPR003065; Ig_WEC.
InterPro; IPR003596; Ig_V.

SMART; SM00406; IGY; 1.

SMART; SM00406; IGY; 1.

SMORT; SM00405; IGY; 1.
                                                                                                                                                                                                                                                                                        DOMAIN
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Steiner L.A., Lopes A.D.;
"The crystallizable human myeloma protein Dob
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steiner L.A., Garcia Pardo A., Margolies M.N.;
"Amino acid sequence of the heavy-chain variable region
crystallizable human myeloma protein Dob.";
Biochemistry 18:4068-4080(1979).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HUMAN
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P01782;
                                                                                                                                                                                                                                                                                                                                            Immunoglobulin V region.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last anoutation
19 heavy chain V-III region DOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- MISCELLANEOUS: THIS GAMMA-1 MYELOMA PROTEIN HAS A DELETION HINGE REGION. THERE ARE NO LIGHT-HEAVY OR INTER-HEAVY CHAIN DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=80020921; PubMed=114209;
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117
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                                                                                                                                             \vdash
                                                                                                                                                                                                                                     Similarity
                                                                  TVSS 160
                                                                                                                                           EVQLVESGGDLVQPGRSLRLSCAASGFNFHEYNMHWLRQGPGKGPEWVSTITWNGGSVLY
                                                                                                                                                              EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                                                                                                                                                        120
120 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                      120
13440 MW;
                                                                                                                                                                                                                26.0%; Score 424.5;
67.7%; Pred. No. 5.66
tive 10; Mismatches
                                                                                                                                                                                                                                                                                                                              IG-LIKE
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                                                                                                                                                                                                                                                                                        880DDE307C4B2627 CRC64;
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RESULT 8
HV3B_HUMAN
ID HV3B_H
AC P01763
AC P01763
DT 21-JUL
DT 15-SEP
DE IG head
OS Homo s
OC Eukary
OC Mammal
OX NCBI_T
RN (1)
RP SEQUEN
RA MEDLIN
RA GON1 F
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HV3G.HUMA
ID HV3G
AC P011
DT 21---
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DT 15---
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21-JUL-1986 (Rel. 01, Last seque
15-SEP-2003 (Rel. 42, Last annot)
Ig heavy chain V-III region CAM.
Homo sapiens (Human).
                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOD_RES
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
                                                                                                                                                                       21-JUL-1986 (Rel. 01, Create
21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
                                                                                                                                                                                                                                                                 HV3B_HUMAN
P01763;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239-3243(1980)
-!- MISCELLANEOUS: THIS MU CHAIN WAS ISOLATED FR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             باسمعلیموره; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PATIENT WITH MACROGLOBULINEMIA.
-!- SIMILARITY: Contains 1 immunogl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                        MEDLINE-83273707; PubMed=6410398
                                                                                                                                                       Homo sapiens
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Lehman D.W.;

"Amino acid sequence of the variable region of a

"Amino acid sequence of the variable region of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81013859;
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GO:0003823; F:antigen binding activity; NAS
GO:0006955; P:immune response; NAS.
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obulin V region; Pyrrolidone carboxylic
1 112 IG-LIKE.
1 1 1 PYRROLIDONE CARBOX)
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122 AA;
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                                                                                                                                                       (Human)
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                                                                                                            Chordata;
Primates;
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Last annotation 
region WEA.
                                                                                                                                                                                                                                           Created)
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                                                                                                       Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                        PRT;
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HV3D_HUMAN
ID HV3D_H
AC P01765
DT 21-JUL
DT 15-SEP
DE Ig hea
OS Eukary
OC Eukary
OC Mammal
OX NCBI_T
RN [1]
RP SEQUEN
RX MEDLIN
RX MEDLI
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Best Local S
Matches 84
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Interpro; IPR003006; I;
Interpro; IPR003596; I;
Interpro; IPR003596; I;
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                               "ImmunoJobulin structure and genetics.
regions of a mu and a gammaz chain.";
J. Biol Chem. 252:7192-7199(1977)
-1- MISCELLANEOUS: THE SEQUENCES OF THE
OF IGM AND IGGZ ISOLATED FROM A SING
GAMMOPATHY ARE IDENTICAL. THEIR LIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region TIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HV3D_HUMAN P01765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence of the Fv region of a human monoclonal IgM (protein MEA) with antibody activity against 3,4-pyruvylated galactose in Klabsiella polysaccharides K30 and K33.";
Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY AGAINST 3,4-PYRUYLATED CALACTOSE AND ISOLATED FROM A PATIENT WITH WALDENSTROM'S MACROGLOBULINEMIA.
                                                                                                                     PIR; A02048; H3HUTL.
HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=78005528; PubMed=409716;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART; SM00406; ĪGV; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Pyrrolidone
Immunoglobulin V 112

IG-LIKE.

DOMAIN 1 112

IG-LIKE.
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                                                                                                                                                                   -!- SIMILARITY: Contains
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mammalia; Eutheria;
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                             InterPro;
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GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activity; GO:0000585; P:immune response; NAS. erPro; IPR007110; Ig-11ke. erPro; IPR003006; Ig_MHC.
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GO:0003823; F:antigen binding
                                                                                                                                                                                              IDENTICAL.
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84; Conservative
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114 AA;
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12256
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69.4%;
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                                                                                                                                                                      immunoglobulin-like
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Pred. No. 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PYRROLIDONE CARBOXYLIC ACID
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g activity;
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RESULT 10
HV31.HUMAN
ID. HV31.HUMAN

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Best Local S
Matches 83
GO; GO:0005576; C:extracellular; NAS.
GO; GO:000576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0077110; Ig-like.
InterPro; IPR003706; Ig-MHC.
InterPro; IPR003596; Ig-V.
InterPro; IPR003596; Ig-V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PR0SITE; PS50835; IG_LIKE; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic ac.
DOMAIN
1 112 IG-LIKE.
DOMAIN
1 112 IG-LIKE.
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21-JUL-1986 (Rel. 01, Last s
21-JUS-2003 (Rel. 42, Last a
15-SEP-2003 (Rel. 42, Last a
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P01770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ponstingl H., Hilschmann N.;
"The rule of antibody structure. The primary structure monoclonal IgG1 immunoglobulin (myeloma protein Nie). I chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
                                                                                                                                                                                                                                                                                                                                                                                             Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";

Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
NON_TER
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MEDLINE=77070267; PubMed=1002129;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-77070269; PubMed-826475;
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                SIMILARITY: Contains 1
                                                                                                                                                                                                                                                                                                                      A91668; G1HUNI.
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115
115 AA;
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Last annotation 
region NIE.
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Pred. No. 1
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     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4DCC67D179F62326 CRC64;
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                                                                                                                                                                                                                                                                                                                                                domain.
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Best Local S
Matches 82
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Best Local
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin V region.
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$1701784;
$21-JUL-1986 (Rel. 01, Cre.
$21-JUL-1986 (Rel. 01, Las.
$15-SEP-2003 (Rel. 42, Las.
$15-SEP-2003 (Rel. 42, Las.
$15 heavy chain V region G
$25 Canis familiaris (Dog).
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Biochemistry 16:3160-3168(1977)
                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; (Mammalia; Eutheria; Carnivora; MCBI_TaxID=9615;
                                                                                                                                                                                                                                            interPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                           Wasserman R.L., Capra J.D.;
Primary structure of the variable
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=77242268;
                                                                                                                                                                                                                                                                                                                                                                             EQUENCE
                                                                                                                                                                                                                                                                                                   - MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN - SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                             A02067; AVDGGM.; P01772; 2FB4.
114
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                                                    ADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAGRGWYFDLWGKGTTVTVS
                    S 160
                                                                                  EVQLVESGGDLVKPGGSLRLSCVASGITFSGYDMQWVRQAPGKGLQKVAYFNDALSAQGY
                                                                                              EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
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                                         ADAVKGRFTISKDNAKDSLYLQMNSLRAEDTAVYYCAP---
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114
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114 AA;
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119
119 AA;
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                                                                                                                                                                                                                                                                                                                                                                  PubMed-407924;
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42, Last annotation update)
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119
13242 MW;
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                                                                                                                                      25.3%;
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                                                                                                                           Score 412.5;
Pred. No. 3.8e
L1; Mismatches
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Pred. No. 3.7e-23;
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Canis.
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RESULT 12

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Best Local
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                                                                                                                                         P01808;
21-JUL-1986 (Rel. 01, Createu,
21-JUL-1986 (Rel. 01, Last sequence up.
15-SEP-2003 (Rel. 42, Last annotation
-- heavy chain V region T601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSE
HV21_MOUSE
P01790;
          MEDIINE-79223895; PubMed-111245;
Rao D.N., Rudikoff S., Krutzsch H., Potter M.;
"Structural evidence for independent joining reg
immunoglobulin heavy chains from anti-galactan m
its potential role in generating diversity in
complementarity-determining regions.";
Proc. Natl. Acad. Sci. U.S.A. 76:2890-2894(1979)
-1- MISCELLANEOUS; THIS CHAIN WAS ISOLATED FROM
                                                                                                                                                                                                                      MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-JUL-1986 (Rel. 01, Created 21-JUL-1986 (Rel. 01, Last ser 15-SEP-2003 (Rel. 42, Last an 19 heavy chain V region M511.
Mus musculus (Mouse)
                                                                                                              Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                     Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; SMART; SM00406; IG;
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Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                              SEQUENCE
                                                                                                                                                                                                          HV38_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Immunog lobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
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                                                                                                                                                                                                                                                              VSS
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                                                                                                                                                                                                                                                                                                                                             EVKLVESGGGLVQPGGSLRLSCATSGFTFSDFYMEWVRQSPGKRLEWIAASRNKANDYTT
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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122
122 AA;
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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13652 MW;
                                                                                                                         Chordata;
Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                                         Score 409.5;
                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 6.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 IG-LIKE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                             9F4837731EA50207 CRC64;
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RESULT 14
HV3H_HUMAN
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Interpro; leave; 1; 1.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
SMART; PS50835; IG_LIKE; 1
Immunoglobulin V region.
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                                                                                                                   Interrac, IPROUSSA, Interproperty ig; 1.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1
PROSITE; PS50835; IG_LIKE; 1
Interpretation of the second of the sec
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InterPro;
InterPro;
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region GA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SIMILARITY: Contains 1 immunoglobulin-like PIR; A02078; AVMST6. HSSP; P01810; 2FBJ.
                                                                                           MOD_RES
                                                                                                                                                                                                                      GO; GO:0006955; P:immune response; InterPro; IPR007110; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                            MACROGLOBULIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Biochemistry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; C
                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                      GO;
                                                                                                                                                                                                                                                                                                                                           HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                 P; P01772; 2FB4.
GG:0005576; C:extracellular; NAS.
GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NZ
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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 Conservative
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Primates;
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63.6%;
                   24.8%;
62.1%;
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heavy chains
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Pred. No. 7.
                 Score 405.5;
Pred. No. 1.
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                                                                          74E5B6959E84100A CRC64;
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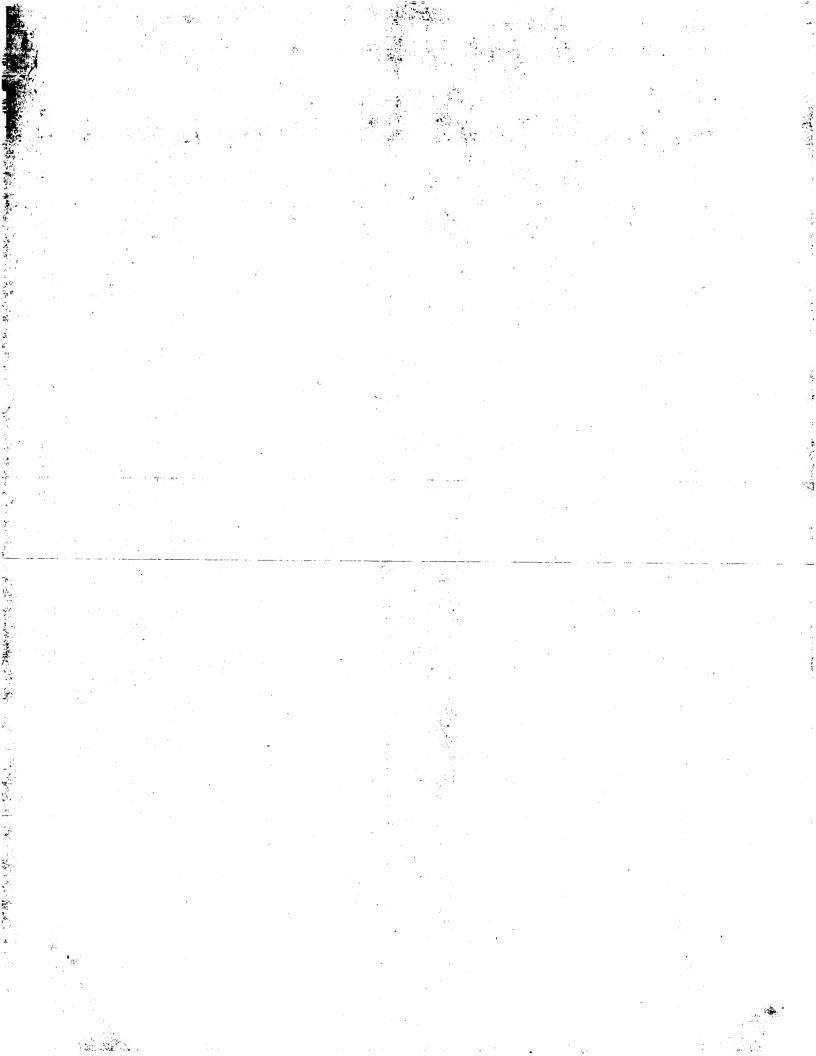
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RESULT 15
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SMART; SM00406; IGv; 1
PROSITE; PS50835; IG_L
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
19 heavy chain V region M603.
                                                                                                                                                                                                                                                                                                    InterPro;
InterPro;
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MEDLINE-80199926; Pubmed-6769593;
MEDLINE-80199926; Pubmed-6769593;
Huang H., Davis M., Calame K., Hood L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF FAB FRAGMENT MEDLINE-75065510; PubMed-4530984; Segal D.M., Padlan E.A., Cohen G.H., Rudikoff S., Pot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Early P., Huang H., Davis M., Calame K., Hood L.;
"An immunoglobulin heavy chain variable region gene is three segments of DNA: VH, D and JH.";
Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; F
                                                                                                                                                                                                     Immunoglobulin
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                    BINDS PHOSPHORYLCHOLINE
-!- SIMILARITY: Contains 1
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-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      binding myeloma protein.";
Biochemistry 13:4033-4038(1974).
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MEDLINE=75017346; PubMed=4213527;
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[1]
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                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rudikoff S., Potter M.;
                                                                                                                                                                                                                                                                                                                                   1MCP; 15-JUL-92.
2MCP; 15-JUL-92.
                                                                                                                                                                                                                                                                                                                                                                        B90795; AVMS63
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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Rodentia;
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                                                                                                                                                                                                                                                                                                                                                                                  immunoglobulin-like domain
                                                                                                                                 H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
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H-BOND WITH THE PHOSPHATE GROUP OF PHOS-
PHORYLCHOLINE.
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13626 MW;
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Pred. No. 1.5e-22;
7; Mismatches 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1;
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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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SP_ARCHea:*

Sp_bacteria

Sp_bacteria

Sp_bacteria

Sp_fungi:*

Sp_fungi:*

Sp_nmann:*

Sp_nmanna

Sp_manna

Sp_manna

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Sp_pha

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Sp_pha

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Sp_pha

Sp_r

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length: 2000000000
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1633
1 MTMITPSFGAFFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
Match
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Gapop 10.0 , Gapext 0.5
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     MTMITPSFGAFFLEIFNVKK......HHHGAAEQKLISEEDLNGAA
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sp_phage:*
sp_plant:*
sp_rodent:*
sp_virus:*
sp_virus:*
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sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
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sp_mammal:*
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241
107
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11 Q921A6
4 Q9NSA6
4 Q9NSK6
4 Q9RCC1
11 Q925C1
11 Q925C1
4 Q8TC77
4 Q9UL71
4 Q8WUX1
11 Q96BB9
4 Q9UL90
11 Q91WP5
11 Q99KA4
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1580.572 Million cell updates/sec
Q8wu38 homo
Q8tc77 homo
Q9tc77 homo
Q9u171 homo
Q9u171 homo
Q9u190 homo
Q9u190 homo
Q9u190 homo
Q9u190 homo
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Q9u191 homo
Q9u191 homo
Q9u191 homo
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Q921a6 mus
Q9nsd6 homo
Q9nsd6 homo
Q8n5k4 homo
Q9hcc1 homo
Q925s1 mus
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s musculu
sapien
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                                               Qy
                                                                                                              Query Match 54.4%; Score 888.5; DB 11; Best Local Similarity 61.4%; Pred. No. 3.5e-59; Matches 180; Conservative 29; Mismatches 67;
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| SEQUENCE FROM N.A. STRAIN-Balb/C; TIS MEDLINE-20183931; Shinohara N. Demu "Isolation of a va recognizing a cell method."; Proc. Natl. Acad. EMBL; AB036341; BA HSSP; P01607; 1REI InterPro; IPR00309 InterPro; IPR00309 Pfam; SM00406; 19; SMART; SM00406; 19; SMART; SM00406; 19; PROSITE; P550835; SEQUENCE 298 AA;  | ČN 8. Mus musculus Eukaryota; M Eukaryota; Eu Mammalia; Eu NCBI_TaxID=1 | 01-MAY-2000<br>01-MAY-2000<br>01-MAY-2000<br>01-MAR-2003<br>CN 8 SCFV. | 1<br>DYFO    |            | 17, 439.5<br>119, 439.5<br>119, 434.4<br>119, 434.4<br>125, 425.7<br>226, 425.7<br>227, 425.7<br>228, 424.5<br>229, 419.5<br>249, 419.5<br>249, 419.5<br>249, 419.5<br>259, 419.5<br>269, 419.5<br>271, 272.7<br>271, 272.7<br>271, 272.7<br>271, 272.7<br>272, 272.7<br>273, 273.7<br>273, 273.7<br>273, 273.7<br>273, 273.7<br>273, 273.7<br>274, 274.7<br>275, 275.7<br>275, 27 |
|--|---|--|--------------|------------|--|
| CEE FROM N.A.  Balb/c; TISSUE  Balb/c; TISSUE  Ball/c; TISSUE  Ball/c; TISSUE  Ball 8331; pub  Bara N., Demura  tion of a vascu  izing a cell po  atl. Acad. Sci  AB036341; BAA88  P01607; 1REI.  TO; IPR003006;  TO; IPR003096; TO; IPR003596; TO; IP | ·· ·· O   | (TrEMBLrel.<br>(TrEMBLrel.<br>(TrEMBLrel.                              | PRELIMINARY  |            | 2222223.5.5.6.6.6.9<br>222223.5.5.6.00000000000000000000000000000000   |
| TISSUE=Spleen; I; pubMed=1070 I; pubMed=1070 emura T., Fuku vascular cell evascular cell evascular ity k d. Sci. U.S.A. BAA88633.1; REI. Ig-like. 3006; Ig_MHC. 3596; Ig_v. Ig. LIKE; 2. IG_LIKE; 2. AA; 31867 MW;   | ).<br>Chordata;<br>Rodentia;  |  | NARY;        |            | 1233<br>4733<br>1044<br>1044<br>1044<br>1044<br>1049<br>1049<br>1049<br>1049   |
| leen<br>=107<br>Fuk<br>cel<br>ity<br>ity<br>ity<br>ity<br>ity<br>ity<br>ity<br>ity<br>ity  | lata<br>itia  | 13,<br>13,<br>23,  |              |            | 4446644144114114144666444  |
| da H.; wall-specific monoclona y using a phage display 97:2585-2590(2000).   | Craniata; Vertebrata;<br>Sciurognathi; Muridae;                         | Created)<br>Last sequence update)<br>Last annotation update)           | PRT; 298 AA. | ALIGNMENTS | O9UL84 O91Z05 O8TBC9 O8UC16 O9UL87 O9Y509 O8NC16 O96K68 O91XE1 O8N4Y9 O9UL72 O9UL72 O9UL72 O9UL78 O9UL88 O8SF4 O92CE7 O9UL88 O8R3V9 O9UL86 O92SS2 O9UL95 O9UL95 O9UL92 O9UL92 O9UL92 O9UL92 O9UL92 O9UL94 O9UL94 O9UC93  |
| <pre>subtraction subtraction ;</pre>   | Euteleostomi<br>Murinae; Mu   |  |              |            | Q9u184 h Q91z05 Q8tbc9 h Q9u187 h Q9y508 h Q8hc16 h Q9hxe1 Q9hxe1 Q9lz07 Q8n5f4 h Q9lz07 Q8n5f4 h Q9lz08 Q8vea0 Q8vea0 Q8vea0 Q9u194 h Q9u192 h Q9u192 h Q9u194 h  |
| ody<br>tion  | tom1;   |  |              |            | homo homo homo homo homo homo homo homo  |
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|  |   |  |              |            | sapien sapien sapien sapien sapien sapien musculu sapien  |

DB 11; Length 298; Indels

17;

Gaps

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Best Local Sim
Matches 129;
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X Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D A Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D A Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D A Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D A Chung J.H., Choi J.H., Chung H.K.;

A Yi K.S., Suh P.G., Ryu S.H., Chung H.K.;

"Cloning and characterization of cDMAs encoding VH and VL of monoclonal anti-CBA antibody (CEA 79) cross-reactive with NCA generation of a single-chain Fv molecule (scFv).";

Mol. Cells 7:816-819(1997).

Mol. Cells 7:816-819(1997).

Mol. Cells 7:816-819(1997).

R EMBL; U88067; AAB48044.1; -.

R InterPro; IPR003006; Ig-1ike.

R InterPro; IPR003106; Ig-1ike.

R InterPro; IPR003196; Ig-v.

R PAGNITE; SM00406; IGV; 2.

R PAGNITE; PS50835; IG_LIKE; 2.
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2003 (TrEMBLrel. 23, Last annotation update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Anti-CEA 79 single chain Fv fragment (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                           VSSGGGGSGGGGGSDIELTQSPSSLSASLGGKYTITCKASQDINKYIAWYQHKPGK
                                                                                                                                                                                                                                                                    VSSGGGSGGGGGGGSS-ELTQDP-AVSVALGQTVRITCQGDSLRSYYASWYQQKPGQ
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                                                                                               VFGGGTKL 279
                                                                                                                                              GPRSAHTLHIYIQ
                                                                                                                                                                                                                                                                                                                                                                                                                                          QVKLQQSGPELKKPGETVKISCKASGYTFTDYGMNWVKQAPGKGLKWMGWINTYTGEPTY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GSGTQYSLKINSLQPEDFGSYYC -----QHFWTTPYTFGGGTKLEIKRAAA
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241 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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26086 MW;
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52.0%;
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Pred. No. 9.1e-39;
6; Mismatches 63;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63;
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Best Local S
Matches 105
                                        Strausberg R.;
Strausberg R.;
Strausberg R.;
Strausberg R.;
Submitted (JUN-2002) to the EMB
EMBL; BC03224; AAH32249.1; -.
InterPro; IPR003599; Ig-1ike.
InterPro; IPR003597; Ig-21.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00409; IG; 4.
SMART; SM00409; IG; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
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O9NSD6; PREMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8N5K4;
Q1-QCT-2002 (TrEMBLrel.
Q1-QCT-2002 (TrEMBLrel.
Q1-MAR-2003 (TrEMBLrel.
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pı
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Autoimmunity.";
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; L43092; AAA69746.2; -.
HSSP; P01709; 2MCG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein (Fragment).
Homo sapiens (Human)
Eukaryota, Metazoa; Chordata; Cra
Mammalia; Eutheria; Primates; Cai
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM
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SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. TISSUE-Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hohmann A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELTQDPVVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS
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107 AA;
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11306 MW;
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0; Mismatches
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Best Local S
Matches 100
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Best Local
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01-MAR-2001 (TrEMBLrel. 16, Cree 01-MAR-2001 (TrEMBLrel. 23, Lass 01-MAR-2003 (TrEMBLrel. 23, Lass Single chain Fv (Fragment).

Homo sapiens (Human).

Eukaryota Metazoa; Chordata; C. Mammalia; Eutheria; Primates; C.
                                           0925S1, PRELIMINARY;
0925S1,
01-DEC-2001 (TIEMBLIEL 1
01-DEC-2001 (TIEMBLIEL 1
01-MAR-2003 (TIEMBLIEL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

KIKUChi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

KIKUChi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Rikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Rikuchi M., Takeda C., Tsujimoto Y., Asada S., Nagata K.;

Inman synthetic phage display library and characterization.";

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.

EMBL, AB049915; BAB16829.1; -

HSSEP; P01772; 2FB4.

InterPro; IPR003106; Ig_MHC.

InterPro; IPR003106; Ig_MHC.

InterPro; IPR003596; Ig_v.
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Hypothetical
SEQUENCE 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NON_TER
                             MRP5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; 1g; 1
SMART; SM00406; IGv;
PROSITE; PS50835; IG
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       musculus
                             (Fragment)
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Similarity 80.3%;
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112 AA;
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    (Mouse)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IGV; 1.
IG_LIKE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    5
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Last annotation updat
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Pred. No. 1.7e
5; Mismatches
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                                                sequence update) annotation update)
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1.7e-32;
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Query Match
Best Local S
Matches 104
Strausberg R.;
Strausberg R.;
Strausberg R.;
Stausberg R.;
Stausberg R.;
Stausberg R.;
Sco21276; AAH21276.1;
InterPro; IPRO07110; Ig-1ike.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
                                                                                                                                                                                                                 O8WU38

O8WU38;

O1-MAR-2002 (TIEMBLIEL 2

O1-MAR-2002 (TIEMBLIEL 2

O1-MAR-2003 (TIEMBLIEL 2

      pfam;
      PF00047;
      1g;
      2.

      SMART;
      SM00406;
      IGv;
      1.

      PROSITE;
      PS50835;
      IG_LIKE;
      1

      NON_TER
      218
      218

      SEQUENCE
      218
      AA;
      23013

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mechanism of exogenous the repair of intestinal world J. Gastroenterol.
                                                                                             TISSUE=Tonsil;
                                                                                                                                                                     Hypothetical protein.
Homo sapiens (Human).
Tomorora: Metazoa; Chordata;
                                                                                                               SEQUENCE FROM
                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        int. J. Radiat. Biol. Relat. 1988; ARK43733.1; -
EMBL; AFX40168; ARK43733.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
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NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=11819679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MAQVKLQQSGPELKKPGETVRISCKASGYTFTTAGMQWVQKMPGKGLKWIGWINTHSGVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MAEVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGST
                                                                                                                                                                                                                                                                                                                                                           WFQQKPGQPPKLLTYAASKQGSGVPAGLLASGSGTDFSLNI
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                                                                                                                                                           Primates;
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                               EMBL/GenBank/DDBJ
                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
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Pred. No. 1.
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                                                                                                                                                          Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
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A of mice of
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SQ
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RESULT 9
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Best Local S
Matches 101
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Best Local
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InterPro, IPR007110, Ig-like.
InterPro, IPR003006, Ig_MHC.
InterPro, IPR003596, Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC;
Hypothetical protein.
SEQUENCE 573 AA; 62967 |
                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                          Strausberg R.;
Submitted (FEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8TC77
                                                                                                                                                                                                                           Hypothetical SEQUENCE 4
                                                                                                                                                                                                                                                                                                                                            TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8TC77;
                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein. Homo sapiens (Human).
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hes 101;
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112; Conserv
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                                                                            SSGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPV 218
                                                                                                      EVQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYY
                                                                                                                                                       EVQLVQSGGGVERPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVSWNSGALTSGVHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
                                              LVIYGKNNRPSGI----PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN
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                                                                                                                                                                                                                           al protein 471 AA;
                                                                                                                                                                                    Conservative
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                                                                 ·ASTKGPSVFPLAPSSKSTSGGTAALGC---LVKDYFPE-----PV
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Last sequence update)
Last annotation update)
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Pred. No. 9.9e-31;
0; Mismatches 9
                                                                                                                                                                                            Score 495.5;
Pred. No. 2.5
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                                                                                                                                                                                                                        388F7F4CF588660E CRC64;
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                                                                                                                                                                                             .5e-29;
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                                                                                                                                                                                                    DB 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9;
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                                                                                                                                                                                   Gaps
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IG\_LIKE;

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RESULT 10
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Best Local S
Matches 96
     Strausberg R.;
Submitted (DEC-2001) to the EMI
Submitted (DEC-2001) to the EMI
EMBL; BC020240; AAH20240.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 5.
SMART; SM00406; IGv; 1.
                                                                                                                                                                     Q8WUK1
Q8WUK1;
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2002 (TrEMBLrel. 20,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                   NON_TER
NON_TER
SEQUENCE
                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata,
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; ig; 1.
SMART; SM00406; IGV; 1.
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HSSP; P01772; 2F
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrei. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                         SEQUENCE FROM N.A. TISSUE-Tonsil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98277139; PubMed=9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Young D.C
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                    VSS
                                                                                                                                                                                                                                                                                                                                                    EVQLVESGGGVVQPGGSLRLFCAASGFTFDGYAMHWVRQAPGKGLEWVSLISGDGGSTYY
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121 AA;
                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                       160
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                                                                                                                                                                                                                                                                                                                                                                                                                                    121
13154 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    29.0%;
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Last sequence up
                                                                    EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                           Score 473; DB Pred. No. 2.3e B; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                             8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   87:184-192(1998).
                                                                                                                                 Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Catarrhini; Hominidae
                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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296 BB9 ID 096 BB9 ID 
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Best Local S
Matches 112
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 111; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 1
01-MAR-2003 (TrEMBLrel. 2
Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chorc
Mammalia; Eutheria; Prima
                                                                                                                                                                                                                                                                                                      PROSITE; PS50
PROSITE; PS00
Hypothetical
SEQUENCE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00290;
Hypothetical protes
SEQUENCE 613 AA;
                                                                                                                                                                                                                                                                                                                                        Pfam; PF00047; 1g; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
PROSITE; PS00290; IG_MHC; 3
                                                                                                                                                                                                                                                                                                                                                                                                             Submitted OCT-2001) to the EMBL/GenBank/DDBJ EMBL; BC015760; AAH15760.1; -. InterPro; IPR007110; Ig-11ke. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_v.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                JG protein.
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                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28.7%; Score 468; DB 4;
45.3%; Pred. No. 4.1e-27;
vative 21; Mismatches 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chordata;
Primates;
                                                                                                                                                                                                                                                                                                      65039 MW;
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                                                                                                                                                                                                                                             28.4%;
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19,
23,
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GSASAPTLEPLYSCENSPSDTSSVAVGCLAQDFLPDSITFSWK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                             Score 464.5; DB 4
Pred. No. 7.3e-27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                    4FCA3AD8ECE263D9 CRC64;
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                                                                                                                                                                                                                                                                DB 4;
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Best Local :
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                                                                      Q91WP5 PRELIMINARY; PR
Q91WP5; PRELIMINARY; PR
Q91WP5; O1-DEC-2001 (TrEMBLrel. 19, Last
O1-DEC-2001 (TrEMBLrel. 23, Last
O1-MAR-2003 (TrEMBLrel. 23, Last
Hypothetical 51.6 kDa protein.
Mús musculus (Mouse).
Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Rodentia; Sc
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Q9UL90;
Q9UL90;
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2000 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
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SEQUENCE
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SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MU X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
  SEQUENCE FROM N.A.
                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           113
113 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113
; 12437 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
Primates;
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                                                                                                                                                                        Created)
Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 458; DB 4;
Pred. No. 2.9e-27;
0; Mismatches 13
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                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ED57FDD19086D07F CRC64;
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Strausberg R;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ
EMBL; BC013556; AAH13656.1; -.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR0030596; Ig_wHC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.;
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; BC004786; AAH04786.1; -.
HSSP; P01810; 2FBJ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
12-6 kDa protein.
12-7 kDa protein.
13-8 musculus (Mouse).
14-8 musculus (Mouse).
15-9 kDa protein.
15-9 kDa 
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 4.

PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                          Hypothetical
SEQUENCE 41
                                                                                                                                                                                                                                                                                                PROSITE; PS50835; IG_LIKE; 4. PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10090;
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GLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYLQMNSLRAEDTAVYYCAKILGAG
                                                                   KSGKDITTVNFPPALASGGRYTMSSQLTL-PAVECPEGESVKCSVQHDS
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                                                                                                                                                                                                                                                        al protein.
487 AA; 5
                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                      52554 MW;
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                                                                                                                                                                                    27.3%; Score 446.5; 44.8%; Pred. No. 1.:
                                                                                                                                                               Pred. No. 1.3e-25;
4; Mismatches 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                        7DC8E96DB333077B CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation updat
Myosin-reactive immunoglobulin heavy chain variab
                                                                                                                                                                                               InterPro; IPR003596;
Pfam; PF00047; ig; 1.
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                             EMBL; AF035023; AA
HSSP; P01772; 2FB4
                                                                                                                                                                                                                                                                           retus."
                                                                                                                                                                                                                                                                                               Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9UL91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9UL91
                                                                                                                                                                                     PROSITE; PS50835; IG_LIKE;
                                                                                                                                                                                                                            InterPro; IPR007110;
InterPro; IPR003006;
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                                                                                                                                                                                                                                     InterPro;
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ne : 52.449
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                                                                                                                                                                                                                                                      Immunol. Immunopathol. 87:184-192(1998). Apr35023; AAD56259.1; -.
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                                                                            \vdash
                                                                                                                  l Similarity
89; Conserv
                                     TWGKSGKDITTVNFPPALASGGGYTMSSQLTL-PAVECPEGESVKCSVQHDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -RGWY--FDLWGKGTTVTVSSGG
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                                                                                                                                                        118
118 AA;
September
secs
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                         27.18;
74.28;
                                                                                                                                                         12843 MW;
                                                                                                                                                                                                                           Ig-like.
Ig_MHC.
                                                                                                                                                                                                                 Ig_v.
         22,
          2003,
                                                                                                                 Score 442.5; DB 4;
Pred. No. 4.5e-26;
9; Mismatches 19;
                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                    in rheumatic
           15:21:23
                                                                                                                                                                                                                                                                                                        Kalis
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chain variable
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                                                                                                                 Gaps
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Title: Perfect score: Sequence:

US-10-052-798-10 1642

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protein search, using sw model

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September 22, 2003, 15:13:04; Search time 52.2793 Seconds (without alignments) 947.272 million cell updates/sec

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

Searched:

Database

A\_Geneseq\_19Jun03:\*
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2: /SIDS1/gcgdata/gei
3: /SIDS1/gcgdata/gei
4: /SIDS1/gcgdata/gei
6: /SIDS1/gcgdata/gei
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7: /SIDS1/gcgdata/gei
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum Total number

Maximum

DB

seq

length:

2000000000

of hits satisfying chosen parameters:

1107863 seqs, 158726573 residues

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N-PSDB; AAV72533
                                        WPI; 1999-045228/04
                                                                                Adams
                                                                                                                                                              09-FEB-1998;
15-MAY-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Single chain Apo-2 antibody
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                                                                                                                      (GETH
                                                                                                                                                                                                                         14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer;
tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAW83323 standard; Protein;
                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                CW, Ashkenazi AJ,
                                                                                                                    ) GENENTECH INC.
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                                                                                Kim KJ;
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PAMI single chain
Human BLyS binding
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Human antibody fra
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Human Fv molecule
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| >                  | 80                 | 7                    | 6                  | 5                  | 4 1                | ω                  | N                  | 1                  |                          |           | scc<br>and   |
|--------------------|--------------------|----------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------|--------------------------|-----------|--|
| 1231               | 1231               | 1231                 | 1460.5             | 1460.5             | 1460.5             | 1642               | 1642               | 1642               | Score                    |           | ed. No.<br>ore gre<br>d is de  |
| 75.0               | 75.0               | 75.0                 | 88.9               | 88.9               | 88.9               | 100.0              | 100.0              | 100.0              | Query<br>Match           |           | is the<br>ater th<br>rived b   |
| 310                | 310                | 310                  | 309                | 309                | 309                | 312                | 312                | 312                | Query Match Length DB ID |           | number<br>lan or e<br>by analy   |
| 24                 | 23                 | 20                   | 24                 | 23                 | 20                 | 24                 | 23                 | 20                 | BB                       |           | of<br>gua.   |
| ABG74386           | ABB09605           | AAW83324             | ABG74384           | ABB09603           | AAW83322           | ABG74385           | ABB09604           | AAW83323           | ID                       | SUMMARIES | Pred. No. is the number of results predicted by chance to h score greater than or equal to the score of the result bein and is derived by analysis of the total score distribution.                |
| Single chain antib | Amino acid sequenc | , Single chain Apo-2 | Single chain antib | Amino acid sequenc | Single chain Apo-2 | Single chain antib | Amino acid sequenc | Single chain Apo-2 | Description              |           | Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. |

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes human Apo-2 can be used CC therapeutically to induce apoptosis in mammalian cells, and so is useful CC to treat conditions associated with decreased apoptosis e.g. cancer. CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by CD binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It CC can be used to identify agents activating Apo-2, useful to treat CC mammalian cancer cells, and to produce Apo-2 chimeras useful CC therapeutically (e.g. those containing immunoglobulin sequences can be CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope CC antibodies). It can be used to produce antibodies which can be combined CC with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules CC comprising first and second Apo-2 antibodies). Agonistic (especially CC single-chain) antibodies can be administered to induce apoptosis in CC mammalian cancer cells, and antagonistic antibodies used to block CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 CC antibodies may also be used diagnostically e.g. to detect Apo-2 CC expression in cells/tissues and in Apo-2 antibody, designated 20E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human Apo-2 polypeptide inducing apoptosis - useful to to conditions linked with decreased apoptosis e.g. cancer, antibodies to increase or decrease apoptosis
                                            Human; Apo-2;
                                                                                                                                                                            ABB09604 standard;
 Bacteriophage
                               caspase;
                                                                               Amino
                                                                                                              29-MAY-2002
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                                                                            acid sequence of single-chain Apo-2 antibody 20E6.
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                               apoptosis;
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                                                                                                           (first entry)
                             tumour necrosis factor receptor;
tosis; cancer; antibody.
                                                                                                                                                                            Protein;
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Pred. No. 1.6e-101;
); Mismatches 0;
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                                            TNFR; apoptosis;
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Matches
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            ABG74385;
                                    ABG74385 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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09-FEB-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nucleic acids encoding an Apo-2 ligand, useful for activating mulating apoptosis in cancer cells, thus especially useful in tatment of cancer, or in enhancing immune-mediated cell death
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DB; ABL41734.
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                                                                                                                                                                                                                                                                      QMNSLRAEDTAVYYCARDLLKYKGSSSGWFDPWGRGTTVTVSSGGGGSGGGGGGGGGGSSE
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                                     Protein;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15-MAY-1997;
09-FEB-1998;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Apo-2 polypeptides apoptosis in mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Apo-2; tumour necrosis factor family; TNFR; gene therapy; apoptosis; tissue-specific typing; affinity purification; competitive-type receptor binding assay; mouse; 20E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC
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           301
                                     241
                                                             241
                                                                                                              181
                                                                                                                                         121
                                                                                                                                                               121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CW,
                                                                                                                                                                                          61
                                                                                                                                                                                                                  61
                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14; Fig 16; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABX16408
                                                                                                 LTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSG
                                                                                                                                                  QMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVTVSSGGGGGGGGGGGGGGSSE
                                                                                                                                                                                                   CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
KLISEEDLNGAA
                                  SSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAAEQ
                                                                                                                                                                                       CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                       MTMITPSEGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                                                                                                                                                                                          MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                                                                                      QMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVTVSSGGGGSGGGGGGGGSSE
                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                       of anti-apo-2 antibodies.
                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2001US-0052798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-046615P.
98US-074119P.
98US-0079029.
                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SCFV)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and polynucleotides, useful for inducing
cells, in vivo or ex vivo gene therapy,
c assays, or in generating antibodies aga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chuntharapai A,
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Score 1642;
Pred. No. 1.6
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment
                                                                                                                                                                                                                                                                                                       DB 24;
.6e-101;
                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                   312;
                                                                                                                                                                                                                                                                                           0
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                                                                                                                                                                                                                                                                                           Gaps
                                                                                                           240
                                                                                                                                                              180
                                                                                                                                                                                         120
                                                                                                                                                                                                                                         60
                                                                                   240
                                                                                                                                     180
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RESULT 4
AAW83322
IDW AAW8
XXX AAW8
XX AAW8
XXX 
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                                                                                                                                                                                                                                                                        The present invention describes human Apo-2 can be used CC therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. CC Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor CC (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis. It CC can be used to identify agents activating Apo-2, useful to treat CC therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope CC inhibit apoptosis) or diagnostically (e.g. those comprising an epitope CC with a (particularly pharmaceutically acceptable) carrier in compositions CC or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially CC single-chain) antibodies can be administered to induce apoptosis in CC mammalian cancer cells, and antagonistic antibodies used to block CC excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 CC expression in cells/tissues and in Apo-2 antibody, designated 16E2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                Query Match
Best Local S
Matches 282
                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human Apo-2 polypeptide inducing conditions linked with decreased antibodies to increase or decreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 14; Fig 16; 134pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-FEB-1998;
15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; Apo-2; receptor; tumour necrosis factor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW83322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW83322
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO9851793-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6-MAR-1999
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DB; AAV72532.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               301 KLISEEDLNGAA
                           1 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                                                                                              Similarity
MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                standard; Protein; 309 AA.
                                                                                                                                                                                                                                   309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Apo-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          olypeptide inducing apoptosis - useful to treat nked with decreased apoptosis e.g. cancer, and processe or decrease apoptosis
                                                                                                                                                                                                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0020746
97US-0857216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-US09704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody
                                                                                                                                           88.9%;
90.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ę,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          apoptosis; neurodegenerative disease;
TNF; tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chuntharapai
                                                                                                             Score 1460.5; DB 2
Pred. No. 1.9e-89;
3; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim
                                                                                                                                                                       20;
                                                                                                                                                                          Length
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                                                                                                             Gaps
60
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RESULT 5
ABBO9603
ID ABBC
XX ABBO9603
AC ABBC
XX ABBC
XX ABBC
XX Huma
CS AMIR
XX Huma
CS Bact
XX Bact
XX Bact
XX Bact
XX Bact
XX Bact
XX CASS
XX Bact
XX Bact
XX Bact
XX Bact
XX Bact
XX Bact
XX CASS
XX Bact
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
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                                                                 The present sequence represents a single-chain Apo-2 antibody, designated 16E2, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-21). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural
                                                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acids encoding an Apo-2 liq
stimulating apoptosis in cancer cells,
treatment of cancer, or in enhancing in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-MAY-1997;
09-FEB-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; Apo-2;
                                                                                                                                                                                                                                                                                                                                                                   Example 14; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashkenazi AJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriophage.
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)B; ABL41733.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        apoptosis; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QKLISEEDLNGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QKLISEEDLNGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tumour necrosis factor receptor; TNFR; apoptosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97US-046615P
98US-074119P
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                                                                                                                                                                                                                                                                                                                                                              68pp;
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                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antibody.
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                                                                                                                                                                                                                                                                                                                                                                                                                 ligand, useful for activating ls, thus especially useful in t g immune-mediated cell death .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Apo-2 antibody
                                                                                                                                                                                                                                                                                                                 designated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
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Sequence

309

The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating

Example

Fig

16;

64pp; English.

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RESULT 6
ABG74384
ID ABG
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Best Local S
Matches 282
                                                                                                                                          15-MAY-1997;
09-FEB-1998;
14-MAY-1998;
                                                    New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, quantitative diagnostic assays, or in generating antibodies aga Apo-2 -
                                                                                               WPI;
                                                                                                                                                                                                                                 Apo-2; tumour necrosis factor family; TNFR; apoptosis; tissue-specific typing; affinity competitive-type receptor binding assay; mov
                                                                                        N-PSDB;
                                                                                                                                                                                                                                                               single
                                                                                                                                                                                                                                                                                             ABG74384;
                                                                                                                                                                                                                                                                                                           ABG74384 standard;
                                                                                                                                                                        02-NOV-2001;
                                                                                                                                                                                      17-OCT-2002
                                                                                                                                                                                                     US2002150985-A1
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                                                                                                                            (GETH ) GENENTECH INC
                                                                                        2003-198287/19.
DB; ABX16407.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                             Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                        2001US-0052798
                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                          97US-046615P.
98US-074119P.
98US-0079029.
                                                                                                                                                                                                                                                                                                            Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    88.9%;
90.1%;
                                                                                                              AJ,
                                                                                                                                                                                                                                                               (SCFV)
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                                                                                                              Chuntharapai A,
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                                                                                                                                                                                                                                                               fragment
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                                                                                                                                                                                                                                  assay; mouse;
                                                                                                              Kin
                                                                                                                                                                                                                                         gene therapy;
purification;
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Best Loc
Matches
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Human Apo-2 polypeptide inducing apoptosis conditions linked with decreased apoptosis e. antibodies to increase or decrease apoptosis
                                                                    Adams
                                                                                                        09-FEB-1998;
15-MAY-1997;
                                                                                                                                    14-MAY-1998;
                                                                                                                                                        19-NOV-1998
                                                                                                                                                                          W09851793-A1
                                                                                                                                                                                                               TNF
                                                                                                                                                                                                                       Human; Apo-2; re
tumour necrosis
                                                                                                                                                                                                                                                    Single chain
                                                                                                                                                                                                                                                                        16-MAR-1999
                                                                                                                                                                                                                                                                                           AAW83324;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      preparation of
                                                                                      (GETH ) GENENTECH
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                                       1999-045228/04
DB; AAV72534.
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                                                                                                                                                                                                                                                                                                                                                                                                ELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QMNSLRAEDTAVYYCA----KILGAGRGWYFDLWGKGTTVTVSSGGGGSGGGGGGGGG
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                                                                   Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                    Apo-2 antibody
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                        receptor;
is factor;
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                                                                                                        98US-0020746
97US-0857216
                                                                                                                                     98WO-US09704
                                                                                      INC
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                                                                    ĄJ,
                                                                                                                                                                                                                                                                                                                                                                               312
                                                                                                                                                                                                                       apoptosis; neurodegenerative disease;
TNF; tumour necrosis factor receptor;
                                                                   Chuntharapai
                                                                                                                                                                                                                                                    24C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1460.5; DB Pred. No. 1.9e-89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                    useful to treat
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                                                                   ζ
            cancer,
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            and
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           produce
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RESULTI B ABB090 ID ABB090 XX ABB00 XX ABB0 XX

29-MAY-2002

(first entry)

ABB09605

standard;

Protein;

310

AA

Amino acid sequence of single-chain Apo-2 antibody 24C4.

Human;

Apo-2;

tumour

apoptosis;

cancer;

necrosis factor receptor;
cancer; antibody.

US6342369-B1 Bacteriophage caspase;

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in composition or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 therapeutically to induce apoptosis in mammalian cells, and so is used to treat conditions associated with decreased apoptosis e.g. cancer Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR). TNF cytokines can induce apoptosis, thought to be initiated binding to TNFRs, and Apo-2 triggered caspase-dependent apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2 expression in cells/tissues and in Apo-2 purification. The present sequence represents a single chain Apo-2 antibody, designated 24C4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 14; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           present invention describes human
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                                  295
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                                                                                                                                                                                                                                 QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGSGGGGSGGGGGS
                                                                                                                                                                                                                                                                                 CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                                                                                                                                           MTMITESFGAFFLEIFNVKKLLFAIFLVVFFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
                                                                                                                                         QSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV
                                                                                                                                                             -SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                                                                                         MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGVVQPGRSLRLS
                                 HGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                               QMNSLRAEDTAVYYCARD-----RGYYYMDVWGKGTTVTVSSGGGGSGGGSGGGGS
                                                                   PDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
77.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                             15;
 310
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1231; DB 2
Pred. No. 3.3e-74
5; Mismatches 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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RESULT 9
ABG74386
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AC ABG7
XC ABG7
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DT 11-A
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Best Local S
Matches 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24C4,
Apo-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acids encoding an Apo-2 ligand, useful for activating stimulating apoptosis in cancer cells, thus especially useful in treatment of cancer, or in enhancing immune-mediated cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 14; Fig 16; 68pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-MAY-1997;
09-FEB-1998;
Single chain
                                                                       ABG74386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH
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DB; ABL41735.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    resent sequence represents a single-chain Apo-2 antibody, dewhich is isolated from a phage library. It is believed that is a member of the tumour necrosis factor receptor (TNFR)
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                                                                                                                                                                                                                                                                                                                                                                                                                         247;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                              -SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                        CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                           QSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV
                                                                                                                                                                                                                                                                                                                          CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                                                                                                                                             HGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      310 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
antibody (scFv)
                        (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-046615P
98US-074119P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0079029
                                                                       Protein;
                       entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                  75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                                                                                                                                        15;
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1231; D
Pred. No. 3.3e
15; Mismatches
 fragment 24C4
                                                                                                                                                                                                                                                                            ----RGYYYMDVWGKGTTVTVSSGGGGSGGGGSGGGGS
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Matches 247
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09-FEB-1998;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating antibodies, in affinity purification techniques, and in competitive type receptor binding assays when labelled with, for instance, radioiodine, enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a diagnostic for tissue-specific typing. This is the amino acid sequence of the single chain antibody fragment (svFv) 24C4 used in the preparation of anti-apo-2 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, quantitative diagnostic assays, or in generating antibodies aga
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                                                                                                                                                                                                                                                                                                 QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGSGGGGSGGGGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                  CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                                                                                                                                                                                                                                                                                                                                                                                         CAASGETESSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRETISRDNAKNSLYL
                       HGAAEQKLISEEDLNGAA
                                                                                                               PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
                                                                                                                                                                                                                                                                          QMNSLRAEDTAVYYCARD-----RGYYYMDVWGKGTTVTVSSGGGGSGGGSGGGGS
HGAAEQKLISEEDLNGAA
                                                                                          PDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH
                                                                                                                                                                                                            -SELTQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ashkenazi AJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fig 16;
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98US-0079029
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77.7%;
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                                             312
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purification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy, in antibodies against
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                                                                                                            Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated epitope present on cancer cells and important physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardional contents.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lazarovits
Szanthon E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29-DEC-2000;
29-DEC-2000;
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                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to an isolated epitope present on cancer of important in physiological phenomena such as cell rolling, metas inflammation, where the epitope is capable of being bound by an its antigen-binding fragment or its complex comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-DEC-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BIOT-) BIO-TECHNOLOGY GEN CORP
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                                                                                                                                     Similarity
                         AAQPAMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQ
AAQPAMAEVQLVESGGGVVRPGGSLRLSCAASGFTFDDYGMSWVRQAPGKGLEWVSGINW
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                                                                                                                                                                                                                     277
                                                                                                                                                                                                                                                                         the invention.
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Richter
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Amit B,
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pred. No. 8.56
5; Mismatches
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Kooperman L,
                                                                                                      DB 23;
3.5e-72;
les 19;
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CC Important in physiological phenomena such as cell rolling, metastasis and confinammation, where the epitope is capable of being bound by an antibody, its antigen-binding fragment or its complex comprising at least one continuous or its binding fragment having a first hypervariable region. The epitopes are useful for inhibiting cell rolling, inflammation, autoimmune consists, thrombosis, restenosis, metastasis, growth and/or replication of tumour or leukaemia cells, increase in number of tumour or leukaemia cells, increase in number of tumour or leukaemia cells in a patient, cell-cell, cell-matrix, platelet-matrix, for increasing mortality of tumour or leukaemia cells, for increasing mortality of diseased cells to damage by anti-disease, anti-cancer or anti-leukaemia agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for the above mentioned purposes. The epitopes are useful for diseasent for the above mentioned purposes. The epitopes are useful for diseased.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; antibody; epitope; cancer; tumour; cell rolling; inflammation; metastasis; hypervariable region; autoimmune disease; thrombosis; restenosis; leukaemia; inflammatory disease; cardiovascular disease; myocardial infarction; retinopathic disease; abnormal platelet functisulphated tyrosine-dependent protein-protein interaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular inflammatory or cardiovascular inflammatory.
                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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29-DEC-2000;
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Amit B,
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Kooperman
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vogel T, .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levanon
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RESULT 12
ABG78150
ID ABG78
XX ABG78
AC ABG78
XX Humar
XX Humar
XX Humar
XX Humar
XX Homo
OX Homo
OX Homo
OX Homo
OX Homo
ID O1-Al
XX (BIO'
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                                                                                                                                                                                                                                      Hagai Y,
Plaksin |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   treating diseases such as cancer, leukaemia, autoimmune diseases, inflammatory diseases, cardiovascular diseases such as myocardial infarction, retinopathic diseases and other diseases mediated by abnormal platelet function and diseases caused by sulphated tyrosine-dependent protein-protein interactions. This sequence represents a human antibody fragment of the invention.
                                                                                                       Novel peptide/polypeptide for cancer therapy has Fv molecule, construct or fragment, or construct of fragment with enhanced binding characteristics so as to selectively bind target cell in favour of othe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; Fv molecule; hypervariable region; single chain Fv; cytostatic; disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma; leukaemia; adenoma;
                                            Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                          31-DEC-2001;
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                                                                                                                                                                                                                                                                                                       (BIOT-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  lymphoma; myeloma;
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  invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN
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                                                                                                                                                                                                                                      Lazarovits, Peretz T;
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  relates
                                            155-156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  blastoma;
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Pred. No. 8.5e-72;
7; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seminoma;
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polypeptide comprising
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                                                                                                                                                                                                                                                             Szanton
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                                                                                                                                                                                                                                                             Levanon
  an
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                                                                                                       of other
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RESULT 13
ABG78328
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CC molecule, a construct or fragments or a construct of a fragment with Cc enhanced binding characteristics which selectively and/or specifically CC binds to a target cell in favour of other cells, where binding is comparable region and Fv is a single CC primarily determined by a first hypervariable region and Fv is a single CC chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in CC association with or attached, coupled, combined, linked or fused to a cC pharmaceutical agent, is useful in the manufacture of a medicament, where CC the medicament has activity against a diseased cell, preferably a cancer CC cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, CC myeloma, blastoma, seninoma, and melanoma, where the leukaemia cell is an CC acute myeloid leukaemia cell). The peptide is also useful for preparing a CC composition for use in inhibiting the growth of a diseased or cancer Ccell. This sequence represents a human Fv molecule hypervariable region CC related peptide of the invention.
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Best Local S
Matches 238
                                     Hagai Y, I
Plaksin D,
                                                                                                                                                                                                                                                  Human; Fv molecule; hypervariable region; single chain disulfide Fv; dsFv; scFv; cancer; carcinoma; sarcoma;
                                                                                                                                31-DEC-2001;
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                                                                                                       29-DEC-2000;
                                                                             (BIOT-)
                                                                                                                                                                                                                                      lymphoma;
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            2002-619166/66
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                                                                             BIO-TECHNOLOGY GEN CORP
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                                                                                                                                                                                                                                      p Fv; dsFv;
myeloma;
                                                                                                                                                                                                                                                                                            molecule
                                                                                                                                                                                                                                                                                                                                                                         standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WGQGTLVTVSRGGGGGGGGGGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lazarovits, Peretz T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             277
                                                                                                                                2001WO-US49440
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                                                                                                       2000US-0751181.
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                                                                                                                                                                                                                                                                                            hypervariable
                                                                                                                                                                                                                                         blastoma;
                                                                                                                                                                                                                                                                                                                                                                          Protein;
                                                   ç
                                                    Guy
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Pred. No. 8.5e-72;
5; Mismatches 19;
                                                    ₽,
                                                                                                                                                                                                                                                                                          region related
                                                                                                                                                                                                                                                                                                                                                                          B
                                                   Lipschitz
                                                                                                                                                                                                                                         melanoma;
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                                                                                                                                                                                                                                                     ngle chain Fv; cytostatic; sarcoma; leukaemia; adeno
                                                                                                                                                                                                                                                                                            peptide
                                                     Szanton
                                                                                                                                                                                                                                         acute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  312
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                                                                                                                                                                                                                                       myeloid
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                                                     Levanon
                                                                                                                                                                                                                                          1; adenoma;
leukaemia.
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RESULT 14
ABP45459
ID ABP45
XX ABP454
AC ABP45
XX 19-AU
XX 19-AU
XX Unmar
XX ELUMOU
KW LUMOU
KW Immur
KW STALL
KW SYSTE
KW SYSTE
KW COMMAR
XX HOMO
XX 10-JJ
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to a peptide or polypeptide comprising an Fv molecule, a construct or fragments or a construct of a fragment with enhanced binding characteristics which selectively and/or specifically binds to a target cell in favour of other cells, where binding is primarily determined by a first hypervariable region and Fv is a single chain Fv (scFv) or a disulfide Fv (dsFv). The peptide, optionally in association with or attached, coupled, combined, linked or fused to a pharmaceutical agent, is useful in the manufacture of a medicament, where the medicament has activity against a diseased cell, preferably a cancer cell (selected from carcinoma, sarcoma, leukaemia, adenoma, lymphoma, myeloma, blastoma, seminoma, and melanoma, where the leukaemia cell is an acute myeloid leukaemia cell; The peptide is also useful for preparing a composition for use in inhibiting the growth of a diseased or cancer cell. This sequence represents a human Fv molecule hypervariable region
                                                                                                                                     immunosuppressive; immunostimulant; immunomodulatory; ar
antiAIDS; vaccine; cancer; immune; autoimmune disorder;
                                                                                                                                                                       BLys; B lymphocyte stimulator;
tumour necrosis factor; B cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or fragment, or characteristics
                                                                                                                      systemic lupus erythematosus;
                                                                                                                                                                                                                                                               19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                  WO200202641-A1
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                                                                     Homo
                                                                   sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           238;
                                                                                                                                                                                                                          BLyS binding
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                                                                                                      variable
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                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                        HVVFGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN
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                                                                                                      immunodeficiency;
                                                                                                                                                   stimulator; TNF superfamily; human; cytostatic; ptor; B cell proliferation; B cell differentiation; immunostimulant; immunomodulatory; antirheumatic;
                                                                                                                                                                                                                                                                                                                                  Protein;
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Pred. No. 8.5e-72;
7; Mismatches 17;
                                                                                                    rheumatoid arthritis; CVID; AIDS;
ncy; acquired immunodeficiency syndrome
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Best Local Similarity
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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
04;-DEC-2002
                                 ABG92024 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                          This invention describes novel antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                 ABG92024;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, useful the diagnosis and treatment of cancers and immune disorders \cdot
                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                         the invention.
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                                                                         KLTVLG
                                                                                                       VLVIYGKNNRPSGIPDRPSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVPGGGT
                                                                                                                                                 VSSGGGGSGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAP 220
                                                                                                                                                                         DSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDFYDILTGYHDAFDIWGRGTMVT
                                                                                                                                                                                                         VQLVQSGGGLVQPGRSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
                                                                                                                                                                                                                  VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
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                                                                                        KLTVLG
                                                                                                                                        VSSGGGGSGGGGGGSSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAP
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2001US-276248P.
2001US-277379P.
2001US-293499P.
(first entry)
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                                 Protein; 263
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92.7%;
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The invention relates to an isolated epitope present on cancer cells and CC important in physiological phenomena such as cell rolling, metastasis and CC inflammation, where the epitope is capable of being bound by an antibody, CC its antigen-binding fragment or its complex comprising at least one CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC epitopes are useful for inhibiting cell rolling, inflammation, autoimmune CC disease, thrombosis, restenosis, metastasis, growth and/or replication of CC tumour or leukaemia cells, increase in number of tumour or leukaemia CC cells in a patient, cell-cell, cell-matrix, platelet-matrix, cell-epitopes are useful for increasing the CC gratelet-platelet and/or cell-platelet adhesion or aggregation, for CC increasing mortality of tumour or leukaemia cells, for increasing the CC susceptibility of diseased cells to damage by anti-disease, anti-cancer CC crateling agents, or for decreasing the number of tumour or leukaemia cells in a patient, or in the manufacture of a medicament for CC the above mentioned purposes. The epitopes are useful for diagnosing and CC inflammatory diseases such as cancer, leukaemia, autoimmune diseases, CC inflammatory diseases, cardiovascular diseases such as myocardial CC infarction, retinopathic diseases and other diseases mediated by abnormal CC platelet function and diseases caused by sulphated tyrosine-dependent correction interactions. This course care as a striked.
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Matches 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein-protein interactions. This sequence represents protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel isolated epitope present on cancer cells and important in physiological phenomena such as cell rolling, metastasis and inflammation, for treating autoimmune, inflammatory or cardiovascular diseases, and cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 50; 310pp; English.
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Kooperman L,
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Search completed: September Job time: 53.2793 secs 22, 2003, 15:18:44

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APPLICANT: Adams, Camilia W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                 Query Match
Best Local Sim
Matches 312;
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                                                                                                                                                                                                                                                                    TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                   PILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION UNMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb 1
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                             TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
ZIP: 940
                                                                                                                                                                                                                                  TYPE: Amino Acid
                                                                                                                                                                                                                  TOPOLOGY:
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CITY: South San Francisco
STATE: California
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US-09-188-082-16
US-09-184-088-16
US-09-102-716-16
US-09-554-765-2
US-08-918-148-74
US-08-918-148-79
US-08-918-148-34
US-08-918-34-34
US-08-958-140-2
US-08-958-140-2
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Pred. No. 2.2e-126;
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US-09-079-029-9
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APPLICANT: Adams, Camilia
                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/079
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAISCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 9110
TELECOMMUNICATION INFORMATION:
TELECPHONE: 650/225-5116
                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ashkenazi, Av
APPLICANT: Chuntharapai,
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 14
                                                                                                                                                                                         TYPE: Amino Acid
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Pred. No. 1.4e-111;
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                                                                                                                                                    Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORIX AGENT INFORMATION:
ATTORIX MATSCHAIG, Diane L.
NAME: MATSCHAIG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Chuntharapai, APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDLIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: .IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                             LENGTH: 310 amino acids TYPE: Amino Acid
                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER:
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                                                           CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                       QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGSGGGGSGGGGS 178
                                               CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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Chuntharapai, Anan
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APPLICANT: KNOX, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Millats, W.G.
TITLE OF INVENTION: ANTIBODY
FILE REFERENCE: DYOU19.001AUS
CURRENT APPLICATION NUMBER: US/09/260,527A
CURRENT FILING DATE: 1999-02-26
NUMBER OF SED ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version 3.0
SED ID NO 1
SED ID NO 1
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         Sequence 3, Application US/09260527A
Patent NO. 6228599
GENERAL INFORMATION:
APPLICANT: KNOX, J.P.
APPLICANT: Mikkelsen, J.D.
APPLICANT: Willats, W. G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/09260527A Patent No. 6228599 GENERAL INFORMATION:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: UNKNOWN

PEATURE:
ORGANISM: UNKNOWN

FEATURE:
OTHER INFORMATION: Anti-homogalacturonan specific antibodies from
OTHER INFORMATION: phage display library known as the Synthetic sc
OTHER INFORMATION: Library (#1) from the Centre for Protein
OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK.
TITLE OF INVENTION: ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                            248
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RESULT 6
US-10-039-785-53
**Conuence 53, Af
                                                                                                                          CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR PRIOR APPLICATION NUMBER: 60/323,807
PRIOR PRIOR DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-08-04
PRIOR FILING DATE: 2001-08-05
PRIOR FILING DATE: 2001-08-07
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CURRENT APPLICATION NUMBER: US/09/260,
CURRENT FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 3
LENGTH: 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 6538938
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SOFTWARE:
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically
TITLE OF INVENTION: Receptors
                           NUMBER OF SEQ ID NOS: 66 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
                                                                                PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 2001-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Anti-homogalacturonan specific antibodies se
OTHER INFORMATION: from a naive phage display library known as
OTHER INFORMATION: Synthetic scFv Library (#1) from the Centre
OTHER INFORMATION: Protein Engineering, MRC Centre, Cambridge,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: UNKNOWN
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                268 DSSGNHVVFGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLNGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        183 YASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 YSGS-TYYNPSLKSRYTMSVDTSKNQFSLKLSSVTAVDTAVYYCAR------FH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 QDGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFD 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33 AAQPAMAGVQLVESGGGLVQPGGSLRLSCAASGFTF-SSYWMSWVRQAPGKGLEWVANIK 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P----WGRGTTVTVSSGGGGSGGGGGGSGGGSSELTQDPAVSVALGQTVRITCQGDSLRSY
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                                                                                2001-05-25
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                                                                                                         60/293,473
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Best Local Similarity
Matches 186; Conserv
                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -09-184-658-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Assays for Measurement of Protein Fragments TITLE OF INVENTION: Biological Media FILE REFERENCE: PC9946-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Otterness,
                                           NAME/KEY: DOMAIN
LOCATION: (138)..(152)
OTHER INFORMATION: 15
                                                                                                              NAME/KEY: DOMAIN
LOCATION: (23)..(137)
OTHER INFORMATION: 9A4
                                                                                                                                                                                                                                                   OTHER INFORMATION: OTHER INFORMATION: FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
                                                                                                                                                                               NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: Likely the initiator
                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence FEATURE:
NAME/KEY: DOMAIN LOCATION: (153).
                               FEATURE:
                                                                                                                                                                    FEATURE
                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                         LENGTH: 284
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 TVSSGGGGGGGGGGGGSSE--LTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 DSVKGRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARD-LLKVKGSSSGWFDPWGRGTTV
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(153)..(258)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QSPVLVIYQDNKRPSGIPERFSGSNSGNTATLKISGTQAMDEADYYCLAWDSSADW-VFG
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                                                                                                                                                                                                                                                                   Description of Artificial Sequence: 9A4 \ensuremath{\text{VL}} .
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                                               acid
                                               linker.
                                                                                                                                                                                                peptide; Val at position
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; NAME/KEY: SITE
; LOCATION: (271)...(280)
; OTHER INFORMATION: myc tag.
US-09-184-658-40
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US-09-184-658-63
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SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence 63, Application US/09184658
Patent No. 6030792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                FILE REFERENCE: PC9946-A
CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measure TITLE OF INVENTION: Biological Media
                                                                                                                               NAME/KEY: SIGNAL LOCATION: (1)..(2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Otterness,
                                                                                                      LOCATION: (1)..(22)
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                             ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (262)..(267)
                                           NAME/KEY: DOMAIN LOCATION: (23)..(138) OTHER INFORMATION: 5109
                                                                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                          TYPE: PRT
             NAME/KEY: DOMAIN
                                FEATURE:
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Local Similarity 57.9%;
hes 172; Conservative 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQ
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(139)..(154)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ------GGSLDYWGQGTTLTVSSGGGGSGGGGGGGGGQIVLTQSPVFMSASPGEKV
                                                                                                    pCANTAB6
likely in
                                                                                                                                                                               Description scFv.
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                                                                                                      B6 signal peptide; initiator Met.
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                                              domain
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Pred. No. 7.1
                                                                                                                                                                                                                                                                                                                                                                                                         Measurement of Protein Fragments
                                                                                                                                                                                             of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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hes 71;
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: LOCATION: (284)..(289)
: OTHER INFORMATION: His tag.
US-09-184-658-63
                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 9
US-08-564-164A-2
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Best Local Similarity
Matches 179; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                               quence 2, Application US/08564164A tent No. 6159947
                                                                                                         COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTERS STEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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OTHER INFORMATION: 5109
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FILING DALL.

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/FR94/00714

APPLICATION NUMBER: 15-JUN-1994
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LOCATION: (155).
                                                                                                                                                                                                                                                                                                                        APPLICANT: Schweighoffer, APPLICANT: Tocque, Bruno TITLE OF INVENTION: IntraTITLE OF INVENTION: There
                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                     APPLICATION NUMBER: FILING DATE: 28-DEC
                                                                                                                                                                                                                                                ADDRESSEE: Rhone-Poulenc
STREET: 500 Arcola Road,
CITY: Collegeville
                                                                                                                                                                                                                     COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DLLKVKGSSSGWFDPWGRGTTVTVSSGGGGGSGGGGGGGSSE--LTQDP-AVSVALGQT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRITCQ-----GDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTA
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                                                                                                                                                                                                                                                                                                                                        Intracellular Binding Proteins and Use
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3C43
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                                                                                                                                Version #1.30
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33 AAQPAMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSSYMMSWVRQAPGKGLEWVANIKQ 92

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APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CLEMOKINE-TUMOR ANTIGEN FUS
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEO ID NOS: 57
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                                                                                                                                           SOFTWARE: Fas
SEQ ID NO 53
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   Matches
                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                             Sequence 53, Application US/09646028 Patent No. 6562347
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                 LENGTH: 3:
                                                                                  OTHER INFORMATION:
                                                                                                 FEATURE:
                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: ST
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 16-JUN-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Savitzky, Martin F. REGISTRATION NUMBER: 29,6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       153 WGRGTTVTVSSGGGGSGGGGSGGGSS-ELTQDP-AVSVALGQTVRITCQGDSLRSYYAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 AAQPAMAQVKLQQSGGGLVQPGRSLKLSCVVSGFTFSNYGMNWIRQTPGKGLEWVAYISS
                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNHVVFGGGTKLTVLGAAAHHHHHHGAAEQKLISEEDLN 309
                                                                                                                                                                               FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WYQQKPGKSPQLLIYYASSLQDGVPSRFSGSGSGTQFSLKISNMQPEDEGVYYCQQAYKY 256
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   Conservative
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                                                                                  Description
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 49.9%; Score 819.5;
61.8%; Pred. No. 2.9,
tive 23; Mismatches
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Pred. No. 5.3e-60;
                                                                                  of artificial sequence:/note=synthetic
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5; DB 4;
2.9e-59;
hes 62;
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                                                                                                                                                                                                                                                                                           FUSION PROTEINS AS CANCER VACCINES
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   Indels
                              Length 334;
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   19;
 Gaps
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RESULT 12
US-09-646-028-51
; Sequence 51, Appl:
; Patent No. 656234;
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US-09-646-028-55
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SEQ ID NO 55
LENGTH: 339
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Best Local S
Matches 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
GENERAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 55, Appli
Patent No. 6562347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
INFORMATION:
                                                                                                    311
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                                                                                                                    CNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHH 295
                                                                                                                                                                                                                                        DPWGRGTTVTVSS-GGGGSGGGGSGGGGS---SELTQDPAVSVALGQTVRITCQGDSLR-
                                                                                                                                                                             --SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY
                                                                                                                                                                                                                     DGSEKYYVDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWF---
                                                                                                                                                                                                                                                                                                                                        AAQPAMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DPWGRGTTVTVSS-GGGGSGGGGSGGGGS---SELTQDPAVSVALGQTVRITCQGDSLR-
                                                                                                   CQCNDDSLSGWLFGGGTKLTVL---RHHHHHH 339
                                                                                                                                                               GAGYDVNWYQKFPETAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYY
                                                                                                                                                                                                                                                                              SGDTTYYADSVKGRFSASRDNSKNTVYLQMNNLRPNDTAVYFCA-----NNQTGNFCL
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                          Application
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                                                                                                                                                                                                                                                                                                                                                                                                               49.9%; Score 819.5; DB 61.8%; Pred. No. 3e-59;
                           US/09646028
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                                                                                                                                                                                                                                                                                                                                                                                                 62;
                                                                                                                                                                                                                                                                                                                                                                                                                              Length 339;
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; LOCATION: 208
; OTHER INFORMATION: unknown amino
US-08-918-148-78
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; LENGTH: 245
; TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                              Sequence 78, Application US, Patent No. 6342220
GENERAL INFORMATION:
APPLICANT: Adams, Camellia
APPLICANT: W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 51
LENGTH: 348
Query Match
Best Local Similarity
Matches 164; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                         APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/918,148A CURRENT FILING DATE: 1997-08-25 NUMBER OF SEQ ID NOS: 79
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APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS
FILE REFERENCE: 14014.0316/P
                                                                                                                                                        ORGANISM: artificial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 348
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                      NAME/KEY: unknown
                                                                                                                                          FEATURE:
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 Conservative
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48.8%; So 64.8%; Protive 27;
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Score 802; DB 4;
Pred. No. 5.3e-58;
7; Mismatches 52
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Pred. No. 6.5e-59;
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                                Length 245;
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US-08-860-174A-10
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                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/860,174A
FILING DATE: June 16, 1997
PROOR APPLICATION DATA:
APPLICATION NUMBER: EP 95307332.7
FILING DATE: October 16, 1995
APPLICATION NUMBER: PCT/EP/96/03605
FILING DATE: August 14, 1996
INFORMATION FOR SEQ ID NO: 10:
                                                                                                                     Matches
                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                               TYPE: amino acids
TYPE: amino acids
TOPOLOGY: line
WOLFORM
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD, WINDOWS 95, V
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 282 amino acid:
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: VAN DER LOGT, Cornelis Paul Erik
APPLICANT: VERHOELJEN, MARTLINE Elisa
APPLICANT: WILSON, Steve
TITLE OF INVENTION: A BIFUNCTIONAL OR BIVALENT
TITLE OF INVENTION: ANTIBODY FRAGMENT ANALOGUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                           MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ANDHESSEE: PILLSBURY, MADISON & SUTRO LLP
STREET: 1100 New York Avenue, N.W.
STREET: 9th Floor, East Tower
CITY: WASHINGTON. D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: UNITED STATES ZIP: 20005-3918
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TDTYTYYSDNVKGRFTISRDNGKNTLYLQMSSLKSEDTAVYYCARHGYYGK----GYFDY 131
            DGSEKYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDP 152
                                                      AAQPAMAQVQLQESGGDLVKPGGSLTLSCATSGFTFSSYAFSWVRQTSDKSLEWVATISS 75
                                                                        AAQPAMAGVQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQ 92
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                                                                                                                     Conservative
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IUMBER: PCT/EP/96/03605
August 14, 1996
SEQ ID NO: 10:
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                                                                                                                                 48.6%;
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                                                                                                                   26;
                                                                                                                                 Score 798; DB 2;
Pred. No. 1.3e-57;
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GENERAL INFORMATION:
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                                                                                                                                                              Matches
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Best|Local
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                                                                                                                                                                                                                                                                                LENGTH:
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; MOLECULE TYPE: protein US-08-661-052-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Robert Glacian.
APPLICANT: Chezian Somasundaram
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 01
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,4
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
| MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: THE TITLE OF INVENTION: OF UNMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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153 WGRGTTVTVSSGGGGSGGGGSGGGGSS-ELTQDP-AVSVALGQTVRITCQ-GDSL-----
                                                                                                                                                               14, Application US/08661052
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Live 33; Mismatches 66
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US-09-880-748-1470
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; Sequence 10, Application US/10288917
; Publication No. US20030148455A1
; GENERAL INFORMATION:
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             COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION NUMBER: US/10/288,917

FILING DATE: 06-No. US20030148455A1-2002

CLASSIFICATION : UNKNOWN>

PRIOR APPLICATION NUMBER: 10/052798

FILING DATE: 02-NOV-2001

APPLICATION NUMBER: 09/079029

FILING DATE: 14-MAY-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 09-FEB-1998

APPLICATION NUMBER: 60/074119

FILING DATE: 15-MAY-1997

ATTORNEY/AGENT INFORMATION:

NAME: MASSCHARG DIAGRE!
                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESS: ADDRESS: I DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
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Matches 312;
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                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INF
                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: 3.5 inch,
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                           Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                                   PRIOR APPLICATION DATA:
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STATE: California
COUNTRY: USA
                                                                 APPLICATION NUMBER: US/10/052,798 FILING DATE: 02-No. US20020150985A1-2001 CLASSIFICATION: <Unknown>
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                                   APPLICATION NUMBER: US/09/079,029
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Ashkenazi, Avi J.
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Pred. No. 2.8e-109;
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US-10-288-917-9
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Publication No. US20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
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                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NO. US20030148455A1-2002
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLISEEDLNGAA 312
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                                                                                                                                                                                                              CITY: South San F:
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KLISEEDLNGAA 312
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     APPLICATION NUMBER: 10/052798 FILING DATE: 02-NOV-2001
                                                                                                                                                                                             ZIP: 94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Marschang, Diane
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                                                                                                                                                                                                                                                              1 DNA Way
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Pred. No. 2.8e-109;
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US-10-052-798-9
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TELECOMMUNICATION: INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                   COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
                                                                                                                                                                                        TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                              AL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
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        OPERATING SOFTWARE:
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                                                                                                                             STREET: 1 DNA Way
CITY: South San Francisco
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FILING DATE: 14 MAY 1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
                                                                                                 COUNTRY:
                                                                                                                STATE: California
                                                                                                                                                                                                                                                                                                                                                                                            QKLISEEDLNGAA 309
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                                                                                   ZIP:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 15-MAY-1997
                                                                                                                                                           ADDRESSEE:
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90.1%;
      (Genentech)
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"BER: P1101R2D1C1
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US-10-288-917-11
; Sequence 11, Application US/10288917
; Publication No. US20030148455A1
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Matches 282;
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APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                     TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
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                                                                                                                                                                                                                                                                                                                                                                          QKLISEEDLNGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 309 amino acids TYPE: Amino Acid TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                     Chuntharapai, Anan
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90.1%;
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RESULT 6
US-10-052-798-11
Sequence 11, Application US/10052798
Publication No. US20020150985A1
PENERAL INFORMATION:
GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity Matches 247; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South ~
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: WinPatin CURRENT APPLICATION DATA
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NAME: Marschang, Diane L.
                                                                                                                                                                                                                                                             APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTMITPSEGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGSGGGGGGGGG 178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HGAAEQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGI 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: Amino Acid
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TELEFAX: 650/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 310 amino acids
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Pred. No. 4.5e-80;
5; Mismatches 42
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                                                                                                                                                                                                ; Sequence 1470, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
APPLICANT: RUBEN et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind
; FILE REFERENCE: PF523
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                           CURRENT APPLICATION NUMBER: US/09/880,748 CURRENT FILING DATE: 2001-06-15 PRIOR APPLICATION NUMBER: 60/212,210 PRIOR FILING DATE: 2000-06-15 PRIOR APPLICATION NUMBER: 60/240,816 PRIOR FILING DATE: 2000-10-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 650/225-54:
TELEPAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
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les 247; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
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FILING DATE: 02-No. US20020150985A1-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: California COUNTRY: USA
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Pred. No. 4.5e-80;
5; Mismatches 42
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1470
LENGTH: 247
TYPE: PRT
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US-09-880-748-1594
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                                                                                                          US-09-880-748-1594
                                                                                                                                                                                                             CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
                                                                                                                                                         NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1594
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1594, Application US/09880748 Publication No. US20030059937A1 GENERAL INFORMATION:
                                                               Query Match
Best Local :
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Best Local 9
                                               Matches
                                                                                                                      LENGTH: 251
TYPE: PRT
ORGANISM: Homo:
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                             Local
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41 VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
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92.7%;
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                                                            Score 1162;
Pred. No. 2
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Pred. No. 2.1e-77
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                                            DB 11;
2.9e-75;
nes 14;
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US-09-880-748-1109
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEO ID NOS: 3239
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LENGTH: 249
TYPE: PRT
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TITLE OF INVENTION: Antibodies that Immunospecifically
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Pred. No. 2.4e-74;
5; Mismatches 14;
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Gaps

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; TYPE: PRT; ORGANISM: Homo sapiens US-09-880-748-952
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US-09-880-748-982
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                                                                        CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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SEQ ID NO 952
LENGTH: 251
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APPLICANT: Ruben et al.
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Best Local :
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NUMBER OF SEQ ID NOS: 3239
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CURRENT FILING DATE: 2001-06-15
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                 PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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2 GGGTKLTVLG 251
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; TYPE: PRT
; ORGANISM: HOMO s
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LENGTH: 256
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SEQ ID NO 982
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                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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NUMBER OF SEQ ID NOS: 3239
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                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
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                        41 VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV 100
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Pred. No. 1.2e-73; 
6; Mismatches 18
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RESULT 14
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US-09-880-748-916
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
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PRIOR APPLICATION NUMBER: 60/277,379
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Sequence 914, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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SEQ ID NO 916
LENGTH: 248
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APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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Similarity 88.8%;
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FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-10-17

PRIOR FILING DATE: 2000-10-17

PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16

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PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21
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US-09-880-748-2112
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; TYPE: PRT '
; ORGANISM: Homo sapiens
US-09-880-748-914
; ORGANISM: Homo sapiens US-09-880-748-2112
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PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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SEQ ID NO 914
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SEQ ID NO 2112
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/293,499 PRIOR FILING DATE: 2001-05-25
                                                  TYPE: PRT
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| Search   | 망              | Qy         | Db   | Qy  | DЪ  | γQ    | Вb   | γ  | Ф   | νQ  | Mato                                     | Que                         |
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| n comple                                       | 232            | 281        | 172  | 221 | 112   | . 161 | 62   | 101  | 2   | 41  | ches 22                                  | Query Match                 |
| Search completed: September 22, 2003, 15:36:24 | 232 KLTVLG 237 | KLTVLG 286 | VLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGT 231 |     | 112 VSSGGGSSGGGSSGETTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAP 171 |       | DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDTTDYWGQGTRVT 111 | DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDP | VQLVQSGGGLVQPGGSLRLSCAASGFTFSSYEMNWVRQAPGKGLEWVSYISSSGSTIYYA 61 | 41 VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV 100 | vative 4; Mismatches 12; Indels 10; Gaps | 69.1%;<br>Similarity 89.4%; |
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RESULT 2
$41374

$1919c chain Fv antibody - mouse
$ingle chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_
C;Accession: $41374
C;Actsaenko, O; Weller, E.W.; Muentz, K.; Conrad, U.
R;Artsaenko, O; Weller, E.W.; January 1994
A:Description: Construction and functional characterizat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed
A; Reference number: A56446; MUID:95229583; PMID:7713873
A; Accession: A56446
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-268 <TANN
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C;Keywords: heterotetramer; i
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                                                                                                                                                                                                                                                                                                                                                                                                                                                SDASPKLWVYYTSHLPPGVPARFSGSGSGNSYSLTISSMEGEDAATYYCQQFTSS--PFT
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$13726
$19666
$25741
$46390
$46390
$736005
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$31598
$311598
$31117
$31117
$31117
$311609
$311609
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Pred. No. 1.4e-41;
8; Mismatches 81;
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81;

Indels Length

11;

Gaps

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275 173

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16-Aug-1996

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submitted to the EMBL Data Library, June 1994
A;Description: Cloning and analysis of IgM anti-thyroglobulin
A;Reference number: S47181
A;Accession: S47184
                                               RESULT 4
$47184
$1 lambda chain - human
I lambda chain - human
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: $47184
R;McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480
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Best Local S
Matches 128
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                                                                                                                                                                                     238 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG
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; Pred. No. 2.4e-32;
37; Mismatches 71
                                                                                                                                                                                                                                                            Score 568; DB; Pred. No. 4.8
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                                                                           21-Jan-2000
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Ig variable region (VDJ) (clone T20-11) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 **sequence_revision 16-Feb-1996 **text_change 23-0;Date: 16-Feb-1996 **sequence_revision 16-Feb-1996 **text_change 23-0;Caccession: I37780; S25474
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37780
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-147 <RESS
A;Cross-references: EMBL:X67943; NID:933578; PIDN:CAA48130.1; PID:93
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region - human C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 *sequence_revision 10-Nov-1995 *text_change 23-Jul-1999 C;Accession: S31675 R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992 A;Description: Mechanisms that generate human immunoglobulin diversity operate A;Reference number: S31585 A;Accession: S31675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-122 <CUIV
A;Cross-references: EMBL:214175; NID:g31015; PI
A;Cross-references: EMBE:214175; NID:g31015; PI
C;Superfamily: immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
E;21-104/Domain: immunoglobulin homology <IMM>
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A;Molecule type: mRNA
A;Residues: 1-108 <MCI>
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Best Local :
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Pred. No.
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.6e-31;
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                         PID: g33579
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RESULT 8
$78486

Ig heavy chain V region (clone FL13-28) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Apr-1998 #sequence_revision 08-May-1998 #text_change 21-Jan-2000
C;Accession: $78486; $31115
R;Raaphorst, F.M.
submitted to the EMBL Data Library, October 1991
A;Reference number: $78486
A;Accession: $78486
A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C. submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity of A;Reference number: $31585
A;Reference number: $31585
A;Recession: $31587
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-136 <CUI>A;Residues: 1-136 <CUI>C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin homology <IMM>
F;31-114/Domain: immunoglobulin homology <IMM>
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$31587

$31587

Ig heavy chain V region - human

C; Species: Homo sapiens (man)

C; Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999

C; Accession: $31587

R; Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VSS 163
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Pred. No. 3.9e-31;
3; Mismatches 7;
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Pred. No. 2.7e-31;
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A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-139 <RESS
A;Cross-references: EMBL:X67908; NID:g33580; PIDN:CAA48106.1; PID:g33581
C;Superfamily: immunoglobulin V region; immunoglobulin homology
                                                                                                                Ig variable region (VDJ) (clone T21-9) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 23-Jul-1999
C;Accession: I37781; S25475
R;Demaison, C.; Chastagner, P.; Theze, J.; Zouali, M.
Proc. [Natl. Acad. Sci. U.S.A. 91, 514-518, 1994
A;Title: Somatic diversification in the heavy chain variable region genes ex A;Reference number: A36876; MUID:94119917; PMID:8290556
A;Accession: I37781
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A;Molecule type: mRNA
A;Residues; 1-110 -GGRT>
A;Cross-references: EMBL:Z18833; NID:g33419; PIDN:CAA79285.1; PID:g939912
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
C;Keywords: heterotetramer; immunoglobulin
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A;Title: Human anti-self antibodies with high specificity from phage display librarie A;Reference number: 336256; MUID:93178448; PMID:7679990
A;Accession: S36272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ig lambda chain v region (clone alpha-THY-29) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36272
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A:Molecule type: mRNA
A:Molecule type: mRNA
A:Residues: 1-4,'L',6-32,'G',34-52,'E',54-73,'K',75-97
A:Cross-references: EMBL:X62965
C:Superfamily: immunoglobulin V region; immunoglobulin
C:Keywords: heterotetramer; immunoglobulin
E:15-98/Domain: immunoglobulin homology <IMM>
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Matches 108
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARD----
                                                                                                                                                                                                                                                                                                                                                                                                                          61 FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNLYVVFGGGTKLTVLG 110
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Pred. No. 6.4e-31;
1; Mismatches 0
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Pred. No. 5.8e-31;
2; Mismatches 6
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RESULT 11
S70444
Ig lambda chain p
C; Species: Homo (
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(;Species: Homo sapiens (man)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change
C;Accession: S70444; S70426
R;Culsinier, A.M.; Fumoux, F.; Fougereau, M.; Tonnelle, C.
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: an early step
A;Reference number: S70442; MUID:93024508; PMID:1383695
                                          Ig lambda chain - human (fragment)
C;Species: Homo sapiens (man)
C;Species: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C;Accession: S38498
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.;
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens
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S38498
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               A; Reference number: S38488
A; Accession: S38498
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F;21-127/Product: Ig lambda chain V region (fragment) #status predicted
F;34-108/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   submitted to the EMBL Data A; Reference number: S70426
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A; Residues: 1-90 <TON>
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A; Residues: 1-127 <CUI>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
A;Status:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL: X53070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: S70426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Tonnelle, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone E29.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;35-118/Domain:
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Best Local Similarity
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Best Local :
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   preliminary
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                                                                                                                                                                                                                                                                                                                                                                              105;
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                                                                                                                                                                                                                                                                                                                           SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPVLVIYGKNNRPSGIPDR
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97.2%;
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                                                                                                                                                                                                                                                                                                                                                                           Score 546; DB 2;
Pred. No. 1.7e-30;
1; Mismatches 2
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Pred. No. 1.8
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Ig lambda chain - nun
C;Species: Homo sapic
C;Date: 06-Jan-1995 #
C;Accession: S38496
                                                                                                                                                                                                        C;Accession: $25748
R;Combriato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A;Title: V(lambda) and J(lambda)-C(lambda)
A;Reference number: $16439; MUID:91257162;
A;Accession: $25748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: DNA
A; Residues: 1-108 <MAR>
A; Residues: 1-108 <MAR>
A; Cross-references: EMBL: 223035; NID: 9414043; PIDN: CAA80570.1; PID: 9414044
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: heterotetramer; immunoglobulin
F; 14-88/Domain: immunoglobulin homology <IMM>
                                                        A;Cross-references: EMBL:X57813; NID:g33725; PIDN:CAA40950.1; PID:g33726 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;148-216/Domain: immunoglobulin homology <IMM>
                                                                                                                                           A; Molecule type: mRNA
A; Residues: 1-233 < COM>
                                                                                                                                                                                                                                                                                                                                    C; Species: Homo sapiens (man)
C; Date: 22-Nov-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:Z23031; NID:g414039; PIDN:CAA80566.1; PID:g414040 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Reywords: heterotetramer; immunoglobulin C;Reywords: heterotetramer; immunoglobulin F;15-89/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-109 <MAR>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human bloc A;Reference number: S38488
                                                                                                                                                                                    A; Status: preliminary; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                Ig lambda chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g lambda chain - human (fragment)
;Species: Homo sapiens (man)
;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
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Best Local :
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93.6%;
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97.2%;
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  Score
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Pred. No. 4.4e-30;
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  530;
No.
                                                                                                                                                                                                                                  gene segments
PMID:1904362
  4e-29;
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.2e-30;
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| Search completed: September<br>Job time : 21.1128 secs | Qy 278<br>Db 227                      | Oy 219<br>Db 171                                  | Oy 165<br>Db 111   | Qy 105<br>Db 62   | Qy 45<br>Db 2  | Query Match<br>Best Local Similarity<br>Matches 115; Conserv                    | A;Molecule type: mRNA<br>A;Residues: 1-233 <jan><br/>A;Experimental source: hydricloma cell<br/>C;Comment: This protein specifically binds the tumor suppressor protein p53. It restores</jan> | R:Jannot, C.B.; Hynes, N.E.  Biochem. Biophys. Res. Commun. 230, 242-246, 1997  A;Title: Characterization of scFv-421, a single-chain antibody targeted to p53.  A;Reference number: JC5322; MUID:97168950; PMID:9016757  A;Accession: JC5322 | p53 specific single-chain antibody Pab421 - human C;Species: Homo sapiens (man) C;Species: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997 C;Accession: JC5322 | RESULT 15 | Qy 238<br>рь 80                                       | Qy 178<br>Db 20  | Matches 10        |
|--|---------------------------------------|---|--|---|--|---|--|---|--|-----------|---|--|-------------------|
| ted: Septen<br>.1128 secs                              | GGTKLTV 284<br>      :<br>GGTKLEI 233 | APVLVIYGI<br>   :  <br>PPRLLIYU                   | GGGSGGGGSGGGSS-ELTQDPA-VSVALGQTVRITCQGDSLRSY-YASWYQQKPGQ<br> | GRFTISRDNAKNSLYLOMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVTVSSG :  :  :  : | ESGGGLVOPGGSLRLSCAASGFTFSSYWMSWVROAPGKGLEWVANIKODGSEKYYVDSVK 104<br>      :   :      :   :   :   :   :   : | 32<br>Similarity 46<br>5; Conservative  | pe: mRNA<br>-233 <jan><br/>L source: h</jan>   | .; Hynes, N<br>hys. Res. C<br>acterization<br>mber: JC53<br>JC5322  | single-chai<br>no sapiens<br>γ-1997 #sec<br>JC5322   |           | FSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG<br> | 78 SSELTQDPAVSVALGQTVRITCQGDSLRSYYASWYQQKPGQAPYLVIYGKNNRPSGIPDR 23<br> | 100; Conservative |
| 22,  | 3 4<br>3 4                            | KNNRPSGIPDR<br>:    :   <br>VSNLESGVPAR           | GGGSS-ELT  | KNSLYLOMN<br> :    ::<br> SNTAYLOLS                                     | GSLRLSCAA<br> ::   <br> ASVKLSCTT  |   | nydricloma<br>specifica  | Ommun. 23<br>On of scrv<br>322; MUID:   | n antibod<br>(man)<br> uence_rev   |           | SEATTGAQA   | SVALGQTVR  |                   |
| 2003, 15:14:58   |                                       | SGIPDRFSGSSSGI<br>  :         <br> SGVPARFSGSGSGS | QDPA-VSV<br>     :: <br>QSPASLAV                             | SLRAEDTA<br>   :   <br>SLTSEDTA   | SGFTFSS)   | Score :<br>Pred. 1<br>6; Misr   | cell<br>lly bind   | 0, 242-3<br>-421, a<br>9716895  | y Pab42:<br>ision 1:   |           | EDEADYY(<br>       <br>EDEADYY(                       | ITCQGDSI<br>IITCQGDSI  | 5; Mismatches     |
| :14:58   |                                       | VTASLTITG <i>!</i><br>:   <br>!DFTLNIHP\          | /ALGQTVRIT   | AVYYCARDLI<br>AVYYC   | WMSWVRQAE  | 32.3%; Score 530; DB 2; I<br>46.6%; Pred. No. 4e-29;<br>tive 36; Mismatches 74; | is the tun   | 246, 1997<br>single-ch<br>); PMID:90  | - human<br>  |           | NSRDSSGNE<br>       <br> NSRDSSGDC                    | RSYYASWYC<br>  :              <br>  RAYYASWYC                          | natches           |
|  |                                       | AQAEDE/<br>:     <br>VEEEDA/                      | rcogd<br>: :<br>scrasks                                      | LKVKGSS   | PEQGLEN<br>PEQGLEN<br>PEGGLEN  | ;<br>74;  | nor sup  | nain ar<br>)16757   | 7 #text  |           | HVVFGGG<br> :   <br> VLFGGG                           | OKPGQA<br>HKPGQA   | 4;                |
|  |                                       | EDEADYYC-NSR<br>         :  <br>EDAATYYCQHIR      | -SLRSY-Y<br>     <br>WSTSGYSY                                | SGWFDPWG:   | VANIKQDG<br>:   :<br>HIGRIDPEN   | Length 233;<br>Indels   | pressor  | ıtibody t   | _change  |           | TKLTVLG   | PVLVIYGK   | 4; Indels         |
| •  |                                       | NDSSGN<br>: : :<br>NELTRS                         | ASWYQ  | RGTTV<br>:   <br>QGTTV  | SEKYY<br>;<br>;<br>;<br>;<br>;   | 22;   | prote  | arget   | 18-Ju  |           | 286<br>128  | (NNRPS   | 0;                |
|  |                                       | HVVFG   |  | TVSSG<br>     <br>TVSSG   | VDSVK<br> <br> <br>TRSSG   | Gaps  | in þ53   | ed to   | 1-1997   |           |   | GIPDR<br> - - -<br>GIPDR   | Gaps              |
|  |                                       | 277<br>226  | 218<br>170   | 164<br>110  | 104<br>61  | 7;  | . It   | p53.  |  |           |   | 237<br>79  | 0;                |
|  |                                       |   |  |   |  |   | restores   |   | · · · · · · · · · · · · · · · · · · ·  |           |   |  |                   |
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|  | 4  | •      | 1<br>1 - J |     |                                       |    |   |   |   |   |                   |   |      | **                              |   |      |        |          |   | -1100<br>1,44 |  |     |  |
|  |  | Care S |            | 1.2 | <i>12</i>                             | K. |   |   | *                                       |   |                   |   |      |                                 |   |      |        |          |   |               |  |     |  |
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| A CONTRACTOR   | a  |        |            |     |                                       |    |   |   |   |   | • गर              |   |      | i<br>i<br>i<br>i<br>i<br>i<br>i |   |      | , (i)  | •        |   |               |  |     |  |
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| 2 1<br>48  |  | :      |            |     |                                       |    | • |   | •                                       |   |                   |   |      |                                 |   |      |        |          |   |               |  |     |  |
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| Š.   |  |        |            |     | ,, 4                                  |    |   |   |   |   |                   |   |      |                                 |   |      |        |          |   |               |  |     |  |
| 7.<br>2  |  |        |            |     |                                       |    |   | •                                       |   |   |                   |   |      |                                 | • |      |        |          |   |               |  |     |  |
| ÷  |  |        |            |     | * '                                   |    |   |   |   |   |                   |   |      |                                 |   |      |        |          |   |               |  |     | 3<br>1   |
| ,  |  |        |            |     |                                       |    |   |   |   |   |                   |   | . ·  |                                 |   |      | **     | <i>:</i> |   | -             |  |     |  |

Title: Perfect score: Sequence:

US-10-052-798-10 1642

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Scoring table:

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protein on:

protein search, using sw model

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GenCore version (c) 1993 - 2003

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September 22, 2003, 15:13:03; Search time 11.7293 Seconds (without alignments) 1250.910 Million cell updates/sec

Minimum DB seq Maximum DB seq

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Total number of hits satisfying chosen parameters:

127863

47026705 residues

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Searched:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database

SwissProt\_41:\*

Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being predicted by analysis of the total score distribution.

printed, рJ

SUMMARIES

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RESULT 1

LV3A_HUMAN

ID 3A_H

AC P01714

DT 21-JUL

RA NCBLIT

RN | [1]

RN | [1]

RN | [2]

R
RESULT 2
HV3T_HUMAN
ID HV3T_HUMAN
AC P01781;
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Matches 100
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NA
GO; GO:0003823; F:antigen binding activity; NA
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003006; Ig_W.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein.
DOMAIN

1
97
IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DV3A_HUMAN STANDARD; PRT; 1901714; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation ig lambda chain V-III region SH. Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-70166723; PubMed-4909564; Titani K., Wikler M., Shinoda T., Putnam F.W.; The amino acid sequence of a lambda type Bence-Jones protein. complete amino acid sequence and the location of the disulfide pridges."; Diem 245:2171-2176/1970
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Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                                                                                           239 SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLG
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                                                                                                            SGSSSGHTASLTITGAQAEDEADYYCNSRDSSGKHVLFGGGTKLTVLG
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11392 MW;
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HV57_MOUSE
HV57_MOUSE
HV22_MOUSE
HV21_HUMAN
HV27_MOUSE
HV24_MOUSE
HV24_MOUSE
HV25_MOUSE
HV25_MOUSE
HV25_MOUSE
HV25_MOUSE
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Pred. No. 1e-3
5; Mismatches
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                   PRT;
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Result

Score

Query Match

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P01714 P01781 P01768

homo homo homo

sapien sapien sapien

Description

436.5 430.5 430.5 427.5 427.5 418.5 418.5 418.5 418.5 418.5

HV3D\_HUMAN HV3F\_HUMAN HV16\_MOUSE

114 126 119 121 121 117 119

HV3K\_HUMAN HV3B\_MOUSE HV3J\_HUMAN HV3C\_HUMAN

HV3I\_HUMAN

HV3H\_HUMAN

3 homo sapien

S homo sapien

B mus musculu

1 homo sapien

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HV35\_MOUSE

P01763 P01771 P01808 P01771 P01771 P01770 P01769 P01778 P01778 P01778 P01778 P01778 P01778 P01778 P01788 P01788 P01788 P01788 P01762 P01794 P01796 P0

mus musculu carassius a rattus norv

HV3N\_HUMAN HV3M\_HUMAN

414 414 413.5 413

HV01\_RAT
HV01\_MOUSE
HV20\_MOUSE
HV3A\_HUMAN
HV25\_MOUSE
HV37\_MOUSE
HV31\_MOUSE
HV31\_MOUSE
HV31\_MOUSE
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HV43\_MOUSE
HV43\_MOUSE
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HV30\_MOUSE

mus musculu
homo sapien
mus musculu
homo sapien

60

homo sapien mus musculu

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412.5 412.5 411.5 410.5 410.6 410 406.5

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RESULT
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21-JUL-1986
15-SEP-2003
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-75059123; PubMed-4803843; Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschmann N.; "The primary structure of a monoclonal IgM-immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the H-chain type), subgroup H III. Architecture of the complete IgM-molecule. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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  Lehman
"Amino
                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                              HV3G_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                         MEDLINE=81013859; PubMed=6774332;
                                                                 SEQUENCE
                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                          P01768;
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heavy chain V-III region CAM.
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ip; P01772; 2F84.
G0:0005575; C:extracellular; NAS.
G0:0003823; F:antigen binding activity; NAS.
G0:0006955; P:immune response; NAS.
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acid:
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116 AA;
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12730 MW;
                                                                                                                           Primates;
                                                                                                                                          Chordata;
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, Last sequence up
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74.4%;
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variable
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Pred. No. :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE
                                                                                                                         Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2C67CA9AAAAA1282 CRC64;
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                                                                                                                           Hominidae;
of
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human
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  ∄
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chain:
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HV3B_
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                       "Amino acid sequence of the Fv region of a human monoclonal IgM Manino acid sequence of the Fv region of a human monoclonal IgM (protein WEA) with antibody activity against 3,4-pyruvylated galactose in Klebsielia polysaccharides K30 and K33.";

Proc. Natl. Acad. Sci. U.S.A. 80:4837-4841(1983).

-i- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A MONOCLONAL ANTIBODY 1. MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM A PATIENT WITH
                                                                                                                                                                                                                                                                                                   21-JUL-1986 (Rel. 01, Lieuwe, 21-JUL-1986 (Rel. 01, Last sequence up 15-SEP-2003 (Rel. 42, Last annotation 15-Sep-2003 (Rel. 42, Last annotation New Chain V-III region WEA.
                               InterPro;
InterPro;
                                                       HSSP; P01772; 2FB4.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                       _HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location of a possible JH segment.";
Proc. Natl. Acad. Sci. U.S.A. 77:3239
-!- MISCELLANBOUS: THIS MU CHAIN WAS
PATIENT MITH MACROGLOBULINEMIA.
                      InterPro;
                                                                                                      PIR; A02046; M3HUWE.
                                                                                                                                                                                                                              MEDLINE=83273707; PubMed=6410398;
                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                           HV3B_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region; P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A02051; M3HUAM.
                                                                                                                   -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activity; GO:0006955; P:immune response; NAS.
                                                                                                                               AGAINST 3,4-PYRUVYLATED GALACTOSE AND WALDENSTROM'S MACKOGLOBULINEMIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           161
                                                                                                                                                                                                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
        ; IPR007110; ;; IPR003006; I; IPR003596; I
                                                                                                                                                                                                                                                                                                                                                                                                                                     VSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            VSS
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; IPR003006;
; IPR003596;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BSVKGRFTISRDBSKBTLYLQMNSLRAEBTAVYYCARD-RPLYGBYRA-FNYWGQGTLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYYA
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122 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           163
                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
                                                                                                                                                                                                                                                                             Chordata;
Primates;
                     Ig_MHC.
Ig_v.
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71.5%;
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                                             ig-like
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s.A. 77:3239-3243(1980)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PYRROLIDONE CARBOXYLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
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Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A42D0F17D252F1C2 CRC64;
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No. 2
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                                                                                                                                                                                                                                                                                         Vertebrata;
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                                                                                                                                                                                                                                                                              Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2;
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RESULT 5
HV3K_H
HV3K_H
AC P01772
DT 21-JUL
DT 21-JUL
DT 21-JUL
DT 21-SEP
DE IS HOMNO S
OC EUKARY
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Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
"Three-dimensional structure determination of antibodies.
structure of crystallized monoclonal immunoglobulin IgG1 K
Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
[2]
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Immunoglobulin
DOMAIN 1
MOD_RES
DISULFID
DISULFID
STRAND
STRAND
TURN
STRAND
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P01772;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        x-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-81072295; PubMed-7441755;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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21-JUL-1986 (Rel. 01, Last s
15-SEP-2003 (Rel. 42, Last a
Ig heavy chain V-III region
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                                                                                                                                                                                                                                                                                                                                                                                        J. Mol. Biol. 141:369-391(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                        immunoglobulin molecule Kol and
                                                                                                                                                                                                                                                                                                                                                                                                                                           "Crystallographic refinement and atomic models
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Marquart M., Delsenhofer J., Huber R., Palm
                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                           ;; A02055; G1HÜKL.
;; 2FB4; 12-JUL-89.
;; 2IG2; 12-JUL-89.
G0:000576; C:extracellular; NAS.
G0:0003823; F:antigen binding act
G0:0006955; P:immune response; NA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        112
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                                                                                                                                                                                                                                                                                                                                                                                                          .0-A resolution.
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SSA
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obulin V region; Pyrrolidone carboxylic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
 96
110
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71.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence up
                                                                                                                                       3D-structure; Pyrrolidone carboxylic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12;
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                                                                                                IG-LIKE.
PYRROLIDONE CARBOXYLIC
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HV38_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 90
Intearro; Irnv., g. 1.
Intearro; Irnv., g. 1.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalla; Eutheria; R
NCBI_TaxID=10090;
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STRAND
                                                                                                    InterPro;
InterPro;
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STRAND
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                                                                                                                                                           PIR;
                                                                                                                                                                                                                                                                                                                MEDLINE=79223895;
Rao D.N., Rudikof
                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region T601.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                y, A02078; AVMST6.

p; P01810; 2FBJ.

rerPro; IPR003006; Ig_MHC.

rerPro; IPR003055; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDP--WGRGTT
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1107
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                                                                                                                                                                                                                                                                                                                                   PubMed=111245;
                                                                                                                                                                                                                                                                                                                                                                                                      Chordata;
Rođentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13718
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Pred. No. 8.4e
l3; Mismatches
IG-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .4e-26;
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myeloma pr
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PROTEIN

2

Gaps

100

61

158

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RESULT 7

HV3J_HUMAN

ID JJHI
AC P01771

DT 21-JUL
DT 15-SEP
DE IG heary
OC Mammal
OX NCBI_T
RN MEDLIN
RX MEDRI
CC -!- SI
DR HSSP;
DR GO; GC
DR GO; GC
DR GO; GC
DR Interi
DR Interi
DR Interi
DR Ffam;
DR SMART;
DR SMART;
DR SMART;
DR Pfam;
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FT MOD_RN
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Best Local
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Best Local :
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HSSP; P01772; 2F84.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0005576; C:extracellular; NAS.
G0; G0:0006953; F:antigen binding activity; NAS.
G0; G0:0006955; P:Immune response; NAS.
InterPro; IPR00110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HV3J_HUMAN
P01771;
                                                                                                                                                  MOD_RES
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
                                                                                                                                                                             Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Pyrrolidone carboxylic acid.
DOMAIN 1 112 IG-LIKE.
                                                                                                                                                                                                                                                                                                                                                  MEDLINE-79124695; PubMed-420800; Chiu Y.-Y.H., Lopez de Castro J.A., Pc "Amino acid sequence of the VH region cryoimmunoglobulin IgG Hil.";
                                                                                                                                                                                                                                                                                                                                        Biochemistry 18:553-560(1979)
                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
Ig heavy chain V-III region HIL.
                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                MISCELLANEOUS:
                                                                                                                                                                                                                                                                                                                       PROTEIN
            161
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                                                  101
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                                                                      N
                                                                                                             87;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
    | VSS 163
                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                  DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVT
                               DSVKGRFTISRDNSKRTLYMZMNSLRTEDTAVYYCARDPDILTAFS---FDYWGQGVLVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VKLLESGGGLVQPGGSLKLSCAASGEDESRYWMSWVRQAPGKGLEWIGEINPDSSTINYT
                                                                                                                                                  121
121
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119
                                                                                                            Conservative
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                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                             THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
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13169
                                                                                                                                                 13566 MW;
                                                                                                                     26.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26.6%;
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                                                                                                            12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 437; DB Pred. No. 3.5e 12; Mismatches
                                                                                                                     Score 436.5;
Pred. No. 3.9
                                                                                                                                                                     PYRROLIDONE CARBOXYLIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                   480FC53610EF5DAB CRC64;
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                                                                                                           Mismatches
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on update)
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.5e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
                                                                                                                                                                                                                                                                                                                                                           human myeloma
                                                                                                                      9e-25;
                                                                                                                              DB 1;
                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 119
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                                                                                                                             Length
                                                                                                            Indels
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HV3I_HUMAN
ID HV3I_HUMAN
AC P01770;
DT 21-JUI-1986
DT 21-JUI-1986
DT 15-SEP-2003
                                                                                                                              В
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                                                                                        В
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                                                                                                                                                                    Query Match
Best Local S
Matches 83
 21-JUL-1986
21-JUL-1986
15-SEP-2003
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                           101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN
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                                                                                        81
                                                                                                                             21
                                                                                                                                                41
                                                                                                                                                                    83;
                                                                                                                                                                             Similarity
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117
117
(Rel. 01, Created)
(Rel. 01, Last sequence (Rel. 42, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121
                                                                                                                                                                                                          AA;
                                        STANDARD;
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GC:

CerPro; 1.

AterPro; IPROU-

InterPro; IPRO0359b,

InterPro; IPRO0359b,

Pfam; PFO0047; ig; 1.

SMARF; SMO0406; IGy; 1.

SMARF; SMO0406; IGy I.

R PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Signf

"VAL 20 117

20 >117

117

125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Genew, HGNC:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81101090; PubMed=6450418; Matthyssens G., Rabbitts T.H.; Matthyssens G., Rabbitts T.H.; Structure and multiplicity of genes for the hum "Structure and multiplicity of genes for the hum heavy chain variable region."; Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980)-i- SIMILARITY; Contains 1 immunoglobulin-like d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GO; GO:0006955; P:immune response; NAS. InterPro; IPRO3016; Ig-1ike. InterPro; IPRO3016; Ig_MHC. InterPro; IPRO30356; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; J00236; AAA53516.1; -. EMBL; M35415; AAA58735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ig heavy chain V-III region VH26
DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCAR 137
|||||||||||||
|DSVKGRETISRDNSKNTLYLQMNSLRAEDTAVYYCAK 117
                                                                                                         VQLLESGGGLVQPGGSLRLSCAASGFTFSSYAMSWVRQAPGKGLEWVSAISGSGGSTYYG
                                                                                                                                    VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                   26.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; 3D-structure
                                                                                                                                                                                                             5
                                                                                                                                                                                                                                   Score 433; DB 1;
Pred. No. 6.7e-25;
                                                                                                                                                                                                                                                                                                                                                                     IG HEAVY CHAIN V-III REGION VH26. IG-LIKE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                    E826733F1A3CB0F1 CRC64;
                                                                                                                                                                                                                Mismatches
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Last sequence up

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PRT;

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HV3H_HUMAN
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Best Local S
Matches 84
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G0; G0:0005576; C:extracellular; NAS.
G0; G0:0003823; F:antigen binding activ
G0; G0:00006955; P:immune response; NAS.
InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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DISULFID
NON_TER
SEQUENCE
                                           P01769;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
19 heavy chain V-III region GA.
     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                          HUMAN
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=77070267; PubMed=1002129;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;
Dreker L., Schwarz J., Reichel W., Hilschmann N.;

"Rule of antibody structure. The primary structure of a monoclon IgG1 immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

-I- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG1 MYELOMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure monoclonal IgG1 immunoglobulin (myeloma protein Nie). chymotryptic peptides of the H-chain, alignment of the peptides and discussion of the complete structure."; Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
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                                                                                                             HV3H_HUMAN
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                      VSS 163
                                                                                                                                                                                                                                    DSVKGRETISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVT
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13242 MW;
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Pred. No. le
                                                                                                                                                                                                                                                                                                                                                                                                            IG-LIKE;
PYRROLIDONE
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                                                                                                             PRT;
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                                                           on update)
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Best Local S
Matches 80
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
19 heavy chain V-III region BUT.
                                                                               -i- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A2M(2
REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-i- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                             Torano A., Putnam F.W.;

"Complete amino acid sequence of the alpha 2 heavy
IGA2 immunoglobulin of the A2m (2) allotype ";

Proc. Natl. Acad. Sci. U.S.A. 75:966-969(1978).
                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                    HUMAN
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MART; SM00406; IGv; 1.

MART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1.

Immunoglobulin V region; Pyrrolidone carboxylic acid.

Immunoglobulin V region; Pyrrolidone Carboxylic ACID.

PYRROLIDONE CARBOXYLIC ACID.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
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HSSP; P01789; 1MCP.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE.
MEDLINE=74175307; PubMed=4208843;
                    InterPro;
                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                            MEDLINE=78137069; PubMed=416441;
                                                                                                                                                                                                                        iomo sapiens
                                                                                                                                                                       EQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           !- SIMILARITY: Contains 1
                              GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activ GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activity; GO:0006955; P:immune response; NAS.
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; P01772; 2FB4.
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                                                                                                                                                                                                                                                                                                                                                                  161 VSS 163
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          IPR007110;
IPR003006;
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Primates;
          Ig-like.
Ig_MHC.
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65.0%;
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Pred. No.
                                                                                                                                                                                                     Catarrhini;
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                                         activity;
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Best Local
"Heavy chain variable region contribution antibodies: somatic mutation evident in a Cell 24:625-637(1981).
                                                                                                                     PDB;
                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                      MEDLINE=77100368; PubMed=401950;
Adetugbo K., Milstein C., Secher D.S.;
"Molecular analysis of spontaneous somatic mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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SMART;
                                                                                                                                PIR;
                                                                                                                                         EMBL;
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                                                                                                                                                                                                                                                                                         SEQUENCE OF 17-136.
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21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation updat
Ig heavy chain V region MOPC 21 precursor (
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                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=10090;
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lIGC; 03-JUN-95.
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115 AA;
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Paskind M., Reth
                                                                                                                                                                                                                                                                                                                                                                                                                  Chordata; Craniata; Vertebrata; Euteleostomi;
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Pred. No. 1.0
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RESULT 13
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21-JUL-1986 (Re)
15-SEP-2003 (Re)
Ig heavy chain V
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SEQUENCE
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CONFLICT
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SEQUENCE
                                                                                                                                                                                                                InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                         "Immunoglobulin structure and genetics. Identity between variable regions of a mu and a gamma2 chain.";
J. Biol. Chem. 252:7192-7199(1977).
-i. MISCELLANEOUS: THE SEQUENCES OF THE V REGIONS OF THE HEAVY CHAINS OF IGM AND IGG2 ISOLATED FROM A SINGLE PATIENT WITH BICLONAL GAMMOPATHY ARE IDENTICAL. THEIR LIGHT CHAINS ARE APPARENTLY ALSO
                                                                                                                Immunoglobulin V region.
DOMAIN 1 109
                                                                                                                                                  Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE;
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Mammalia; Eutheria;
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                      InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=78005528; PubMed=409716; Wang A.-C., Wang I.Y., Fudenberg H.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
                                                                                                                                                                                                                                                                      GO:0005576; C:extracellular; NAS. GO:0003823; F:antigen binding activity; GO:0006955; P:immune response; NAS.
                                                                                                                                                                                                                                                                                                                                                                                          IDENTICAL.
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                  Similarity
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                                                                                                                                                                                                            IPR007110; Ig-like.
IPR003006; Ig_MHC.
IPR003596; Ig_v.
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(Rel. 01, Last sequence update)
(Rel. 42, Last annotation updat
ain V-III region TIL.
  Conservative
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Primates;
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L2; Mismatches
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DN -> ND (IN REF. 2).
W -> H (IN REF. 2).
Y -> W (IN REF. 2).
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JH4 SEGMENT
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Matches 83
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Rudikoff S., Barstad P., Potter M., H
Unpublished results, cited by:
Hood L., Campbell J.H., Elgin S.C.R.;
Annu. Rev. Genet. 9:305-353(1975).
                                                                                                                                                                                                                                                        MEDLINE-81197602; PubMed-7231520;
Gearhart P.J., Johnson N.D., Douglas
"IgG antibodies to phosphorylcholine
their IgM counterparts.";
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21-JUL-1986 (Rel. 01,
21-JUL-1986 (Rel. 01,
15-SEP-2003 (Rel. 42,
                                                                        SMART; SM00406; ÍGv; 1.
PROSITE; PS50835; IC_LIKE; 1.
Immunoglobulin V region; Hybridoma.
DOMAIN 1 114 IG-LI
                                                                                                                                                                                                                                                                                                                                                                                                                    Early P., Huang H., Davis M., Calame K., "An immunoglobulin heavy chain variable: three segments of DNA: VH, D and JH."; Cell 19:981-992(1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Size differences among immunoglobulin heavy chains phosphorylcholine-binding proteins."; proc. Natl. Acad. Sci. U.S.A. 73:2109-2112(1976).
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                                                SEQUENCE
                                                                                                                   InterPro; IPR007110; Ig-11ke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig. 1
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                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE (S107)
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MEDLINE-80199926; PubMed-6769593;
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MEDLINE-76222762; PubMed-819932;
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HSSP; P01789; 1MCP.
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-SEP-2003 (Rel. 42, Last annotation update)
heavy chain V regions TEPC 15/S107/HPCM1/HPCM2/HPCM3
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            25.5%;
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Score 418.5;
Pred. No. 7.9e
L4; Mismatches
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Sciurognathi; Muridae;
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21-JUL-1986 (Rel. 01, Last sequence up
25-SEP-2003 (Rel. 42, Last annotation
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
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HSSP; P01772; 2FB4.
G0; G0:0005576; C:extracellular; N;
G0; G0:0003823; F:antigen binding ;
G0; G0:0006955; P:immune response;
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Proc. Natl. Acad. Sci. U.S.A. 71:4
-[!- MISCELLANEOUS: THIS CHAIN WAS
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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P01774;
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||- SIMILARITY: Contains 1 immunoglobulin-like domain
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                                                                                                                                  DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGS--SSGWFDPWGRGTT
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Pred. No. 8.3e
17; Mismatches
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DURING ISOLATION).
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Copyright (c) 1993 - 2003 Compugen
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Q96bb9 homo
Q9ul93 homo
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Q921a6 mus
Q9nsd6 homo
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Q8wuk1 homo
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| 338                | 338.5  | 346.5  | 350    | 351.5              | 357.5              | 362                | 363    | 363    | 366    | 371.5  | 381.5  | 394.5  | 409    | 418                | 421.5  | 424.5              | .5     | 427.5  | 434    | 435.5  | 437.5  | 441    | 442.5  | 445                | 445.5              | 447.5  | 452    | 455                |   |
| 20.6               | 20.6   | 21.1   | 21.3   | 21.4               | 21.8               | 22.0               | 22.1   | 22.1   | 22.3   | •      | 23.2   | 24.0   | 24.9   | 25.5               | 25.7   | 25.9               | 26.0   | 26.0   | 26.4   | 26.5   | 26.6   | 26.9   | 26.9   | 27.1               | 27.1               | •      | 27.5   | 7.                 |   |
| 159                | 119    | 236    | 237    | 112                | 104                | 124                | 237    | 124    | 124    | 107    | 234    | 437    | 484    | 233                | 469    | 521                | 131    | 480    | 233    | 493    | 119    | 112    | 486    | 118                | 473                | 479    | 147    | 573                |   |
| 4                  | 4      | 4      | 4.     | 4                  | 4                  | 4                  | 4      | σ      | 6      | 4      | 4      | 11     | 11     | 4                  | 11     | 4                  | 4      | 11     | 4      | 4      | 11     | 4      | 11     | 4                  | 11                 | 11     | 4      | 4                  |   |
| Q96QS0             | Q9UL94 | Q96E61 | Q8WTU6 | Q9UGP3             | Q9UL87             | Q9UL92             | Q8WUK4 | Q9NOW6 | Q9NOW4 | Q9UL82 | Q8N355 | Q9R1A4 | Q8VEA0 | Q8N5F4             | Q8R3V9 | Q8N4Y9             | Q9UL88 | Q91XE1 | Q8TBC9 | Q8NCL6 | Q920E7 | Q9HCC1 | Q91Z07 | Q9UL72             | Q91Z05             | Q91WP5 | Q9Y509 | 8£0M8Q             |   |
| Q96qs0 homo sapien | homo   | homo   | homo   | Q9ugp3 homo sapien | Q9u187 homo sapien | Q9u192 homo sapien | homo   | oryct  | oryct  | homo   | homo   |        |        | Q8n5f4 homo sapien | mus    | Q8n4y9 homo sapien | OMO    | 1 mus  | homo   | homo   | 7 mus  | homo   | 7 mus  | Q9u172 homo sapien | Q91z05 mus musculu | mus    | homo   | Q8wu38 homo sapien |   |

## Matches Query Match Best Local Similarity InterPro; IPR007110; Ig-11ke. InterPro; IPR003006; Ig\_MHC. InterPro; IPR003596; Ig\_v. InterPro; IPR003596; Ig\_v. Iffam; PF00047; Ig; 2. INTERPROSITE; PS50835; IG\_LIKE; ITERPROSITE; ITERPROSITE; PS50835; ITERPROSITE; ITERPROSIT Q9QYF0 Q9QYF0; Q1-MAY-2000 Q1-MAY-2000 Q1-MAR-2003 Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI\_TaxID-10090; Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590(2000). EMBL; AB036341; BAA88633.1; -. HSSP; P01607; 1REI. Shinohara N., Demura T., Fukuda H.; "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."; STRAIN=Balb/c; TISSUE=Spleen; MEDLINE=20183931; PubMed=10706631; CN 8 SCFV. EQUENCE FROM N.A. 186; 0 (TrEMBLrel. 0 (TrEMBLrel. 3 (TrEMBLrel. Conservative PRELIMINARY; 55.6%; 62.8%; 13, 13, 23, 25; Created) Last sequence update) Last annotation update) Score 913; DB 11; Pred. No. 5.9e-63; 5; Mismatches 65 PRT; E0F96B8A17004317 CRC64; 298 ₿ 65; Length Indels 298; 20; Gaps

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EMBL; U88067; AAB48044.1; -.
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SMART; SM00406; IGv; 2.
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Mammalia; Eutheria;
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HTFGGGTKL
                    VVFGGGTKL 282
                                        KGPRSAHTLHIYIQ----
                                                         QAP----VLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNH
                                                                               TVSSGGGGSGGGGSDIELTQSPSSLSASLGGKVTITCKASQDINKYIAWYQHKPG
                                                                                       TVSSGGGGSGGGGSGGGSS-ELTQDP-AVSVALGQTVRITCQGDSLRSYYASWYQQKPG
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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241 AA;
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Rodentia;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002
01-JUN-2002
01-MAR-2003
                                             Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC024289; AAH24289.1; -
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 4.
SMART; SM00406; IGy; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS50835; IG_LIKE; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8TC77
Q8TC77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003596; Ig_v. pfam; PF00047; ig; 1. SMART; SM00406; IGv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Autoimmunity.";
Submitted (JUL-1995) to tl
EMBL; L43092; AAA69746.2;
HSSP; P01709; 2MCG.
      Hypothetical protein SEQUENCE 471 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. TISSUE=Lymphocytes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein (Fragment). Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9NSD6
                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
[1]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS50835; IG_LIKE;
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IPR003006; Ig_MHC.
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; 11306 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chordata;
Primates;
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Primates;
   51791 MW;
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98.1%;
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23,
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Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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      388F7F4CF588660E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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.6e-35;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OBWUK1; PRELIMINARY;
OBWUK1;
O1-MAR-2002 (TIEMBLIEL 2
O1-MAR-2002 (TIEMBLIEL 2
O1-MAR-2003 (TIEMBLIEL 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chc
Mammalia; Eutheria; Pri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypothetical protein.
SEQUENCE 613 AA; 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                       264
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                                                                                                                                                                                                                                                                                                                                                              VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
                                                                                                                                                                                                                                                    VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
||||||||||||:::: | | |
| VQLVESGGGLVKPGGSLRLSCAASGFTFSSYSMNWVRQAPGKGLEWVSSMSSSSSYIYYA
VCKVQHPNGN
                                                                                                            ASWYQQKPGQAPVLVIYGKNN----RPSGIPDRFSGSSSGNTASLTITGAQAEDEADYY-
                                                                                                                                                                      QGTMVTVSS
                                                                                                                                                                                                       RGTTVTVSSGGGGSGGGGSGGGGSSELTQDPAVSVALG----QTVRITCQGDSL--RSYY
                                                                                                                                                                                                                                                                                                                                      VQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VTVSWNSGALTSGYHTFPAVLQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSN
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                                       -CNSRDSSGN
                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Primates;
  235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         --ASTKGPSVFPLAPSSKSTSGGTAALGC---LVKDYFPE------P
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20,
23,
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                                                                                  KNNSDISSTRGFPSVLRGGKYAATSQVLLPSKDVMQGTDEHV
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 500.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                 GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60C7F5950671E315 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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tches 63;
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RESULT: 7
Q9ULB6
ID Q9UL
AC Q9UL
AC Q9UL
DT 01-w
DT 01-w
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DT 01-w
DE Imun
CS Home
OC Euka
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Matches
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Q925S1;
Q925S1;
Q1-DEC-2001 (TrEMBLrel. 19, CO)-DEC-2001 (TrEMBLrel. 19, CO)-MAR-2003 (TrEMBLrel. 23, IMRP5 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
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Mus musculus (Mouse).
Mus musculus (Mouse).
Metazoa; Chordata;
Metazoa; Rodentia;
                                              Q9ULB6 PRELIMINARY; PRT; 95 AA.
Q9ULB6;
Q9ULB6;
Q9ULB6;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence up
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation
Imunoglobulin heavy chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   int. J. Radiat. Biol. Relat. EMBL, AF240168; AAK43733.1; - FROMOTIO; Ig-like. InterPro; IPR003006; Ig_MHC. InterPro; IPR003596; Ig_V.
Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00047; ig; 2.
SMART; SM00406; IGv; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             qui D., Zeng G., Yan X., Li X., Su C.;
"Cloning of mouse genes related to repairing
of the irradiated mice by treatment with the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50835; IG_LIKE; 1.
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                                                                                                                                                                          175
                                                                                                                                                                                      212 YQQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTI
                                                                                                                                                                                                                                     158 TYTVSSGGGSGGGGSGGGGSS-ELTQDPA-VSVALGQTVRITCQG----
                                                                                                                                                                                                                       115 TVTVSSGGGGGGGGGGGGSDIVLTQSPASLAVSLGQRATISCRASESVDNIGISFMNW
                                                                                                                                                                                                                                                                                        98 YYYDSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGT
                                                                                                                                                                                                                                                                          61 KYAEEFKGRFAFSLETSASTAYLQISNLKNEDTATYFCMR-----WDYDGGFAYWGQGT
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02; Conservative
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 Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                            23013 MW;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                     Score 496;
Fred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Stud. Phys. Chem. Med. 19:71-80(2001).
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Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                            527E4FA8F7982817 CRC64;
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8.7e-31;
hes 68;
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on update)
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irradiation in mice.";
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Best Local S
Matches 97
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Best Local S
Matches 94
                                                                                                                                    InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
PROSTIE; PS50835; IG_LIKE; 1.
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(Fragment).
Homo sapiens (Human).
Homo sapiens (Human).
'`~rvota; Metazoa; Chordata; Cr
'`~rvota; Metazoa; Primates; C
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
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HSSP; P01772; 2F
InterPro; IPR007
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NON_TER
SEQUENCE
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                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Human VH gene sequence.";
Submitted (NOV-1999) to the
EMBL; AB035268; BAA87067.1;
                                                                                                                                                                                                              Clin. Immunol. Immunopathol. EMBL; AF035024; AAD56260.1;
                                                                                                                                                                                                                                                        Wu X., Liu B., Van Young D.C.;
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SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
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01-MAY-2000
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[1]
                                                                                                                                                                                                                                    tetus.
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101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           94;
                                                               97;
                                                                        Similarity
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                                VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSVKGRETISRDNAKNSLYLQMNSLRAEDTAVYYC
DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSGWFDPWGRGTTVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS50835; IG_LIKE;
                   VQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAFIRYDGSNKYYA
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95 AA; 10527 MW;
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                                                             30.1%; ilarity 78.9%; Conservative
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                                                                                                        ΑĄ;
                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin heavy
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                                                                                                        12437 MW;
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98.9%;
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                                                           ; Score 494.5; pred. No. 4.9e 7; Mismatches
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Pred. No. 3.6e-
0; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                     Craniata; Ve
Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
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                                                                                                       ED57FDD19086D07F CRC64;
                                                                                                                                                                                                                                             rheumatic
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                                                                                                                                                                                                                                                                                                                                                                 chain variable
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                                                         4.9e-31;
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.6e-31;
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PTT NEW PP SULTATION OF SULTATI
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ID Q99KAA
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Best Local S
Matches 98
                                                                                                                                                                                  Q99KA4 PRELIMINARY; PRT; 48/ AA.
Q99KA4;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Hypothetical 52.6 kDa protein.
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
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  SEQUENCE FROM Strausberg R.
                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                            Mus musculus (Mouse)
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01-MAY-2000
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                                                                                      NCBI_TaxID=10090;
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EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
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Catarrhini;
                                                                                                                   Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Best Local S
Matches 116
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Best Local S
Matches 113
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EMBL; BC015760; AAH15760.1; -.

InterPro; IPR003006; Ig-1ike.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

Pfam; PF00047; 1g; 5.

PFAm; PF00047; 1g; 5.

PROSITE; PS00835; IG_LIKE; 5.

PROSITE; PS00835; IG_LIKE; 5.

PROSITE; PS00290; IG_MHC; 3.

Hypothetical protein.

SEQUENCE 597 AA; 65039 MW; 4FCA3ADBECE263D9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Cho
Mammalia; Eutheria
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EMBL; BC004786;
HSSP; P01810; 2F
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01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 4.
SMART; SM00406; IGv; 1.
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SEQUENCE 487 AA; 52554 P
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
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NCBI_TaxID=9606;
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                                                                                                                                                               al Similarity
116; Conser
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Query Match
Best Local S
Matches 94
                                                                                                                                                                                                                                          InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PP00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL93 PRELIMINARY; PRT; 116 AA.
Q9UL93;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Homo sapiens (Human).
'``rvota; Metazoa; Chordata; '
'``rvota; Primates;
                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                                                                                                                              Clin. Immunol. Immunopathol. EMBL; AF035021; AAD56257.1; HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-98277139; PubMed-9614934;
MEDLINE-98277139; PubMed-9614934;
                                                                                                                                                                                                                                                                                                                                                                                                                  Wu X., Liu B.,
Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                      "Myosin-reactive autoantibodies in fetus.";
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114
                        161
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                                                                                                       41 VQLVESGGGLVQPGGSLRLSCAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYV 100
                                                     61
                                                                                                                                                                           Similarity
                           VSS
                                                  VSS 116
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116 AA;
                        163
                                                                                                                                                                Conservative
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12434 MW;
                                                                                                                                                                          28.5%;
76.4%;
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                                                                                                                                                             ; Score 468.5; l; Pred. No. 5.3e 5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GSASAPTLFPLVSCENSPSDTSSVAVGCLAQDFLPDSITFS
                                                                                                                                                                                                                                                                                                                                                                         87:184-192(1998)
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                                                                                                                                                                                                                     ODA0348154DD6061 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                   rheumatic
                                                                                                                                                                                                                                                                                                                                                                                                                               Kalis
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les 17;
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                                                                                                                                                                                       Length 116;
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Best Local S
Matches 92
A Strausberg R.;

Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.

REMBL; BC032249; AAH32249.1; -.

R InterPro; IPR003599; Ig.

R InterPro; IPR003599; Ig_cl.

R InterPro; IPR003596; Ig_wc.

R InterPro; IPR003006; Ig_MHC.

R InterPro; IPR003596; Ig_v.

R InterPro; IPR003596; Ig_v.

R InterPro; IPR003596; Ig_v.

R InterPro; IPR003596; Ig_v.

R SMART; SM00407; IG; 4.

SMART; SM00407; IG; 1.

SMART; SM00405; IG; 1.

R PROSITE; PS500359; IG_MHC; 1.

Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O8N5K4; PRELIMINARY;
O8N5K4; O1-OCT-2002 (TrEMBLrel. 22,
O1-OCT-2002 (TrEMBLrel. 22,
O1-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "NEDO human cDNA sequencing project.";
Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AK027379; BAB55072.1;
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Mammary gland;
Isogal T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
Sugawara I
Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara I
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi Yakanahe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninoniya K., Iwayanagi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hypothetical protein SEQUENCE 494 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                      rissue=Blood;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
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Similarity 74.8%;
92; Conservative
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Primates;
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Last
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Pred. No. 5
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5.3e-28;
20;
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Best Local S
Matches 93
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Best Local
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                                                                                                                                                                                                                                                                                                              NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Tin B., Van der Merwe P.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9UL84;
01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Clin. Immunol. Immunopathol. EMBL; AF035030; AAD56266.1; HSSP; P01772; 2FB4.
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Myosin-reactive immunoglobulin heavy
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                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tetus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Fragment)
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119
                                  160
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                                                                                                                                                     N
                                                                                                                                                                                                                                  93;
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                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                   TVSS
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|TVTVSS 146
TVSS
                                                                       DSVKGRFTIFRDNSKNMMDLQMNSLRAEDTAVYYCAKD---ERGRLVGTYFDYWGQGTLV
                                                                                           DSVKGRFTISRDNAKNSLYLQMNSLRAEDTAVYYCARDLLKVKGSSSG-WEDPWGRGTTV
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                                                                                                                                                                                                                                                                                                                                                                       PS50835;
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                              122
122 AA;
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                                                                                                                                                                                                                                Conservative
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122
                                  163
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                                                                                                                                                                                                                                                                                                                                                                     Gv; 1.
IG_LIKE;
                                                                                                                                                                                                                                                                                                              122
13579 MW;
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Primates;
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Hin heavy chain variable
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Pred. No. 8.4e-28;
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                             WPI; 1999-045228/04.
N-PSDB; AAV72534.
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                                                                                                              Adams CW,
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| Human VEGF-2 relat | АВЈ19830 | 24 | 253 | 1      | 1013   |
|--------------------|----------|----|-----|--------|--------|
| n BLyS             | ABP44945 | 23 | 252 | N      | 1015.5 |
| 'n                 | AAB69603 | 22 | 239 | Ņ      | 1015.5 |
|                    | ABP45189 | 23 | 253 | 'n     | 1016   |
|                    | ABJ19834 | 24 | 246 | 'n     | 1017.5 |
|                    | ABP45945 | 23 | 249 | 2      | 1018   |
| Human BLyS binding | ABP45321 | 23 | 251 | 2      | 1020   |
| BLy!               | ABP45967 | 23 | 247 | 2      | 1021   |
| BLy:               | ABP45881 | 23 | 247 | Ņ      | 1021   |
| ВЬУ                | ABP44870 | 23 | 254 | 2      | 1021.5 |
| BLy!               | ABP44944 | 23 | 251 | ٨      | 1023   |
| BLy:               | ABP45748 | 23 | 254 | Ν.     | 1023.5 |
| Human BLyS binding | ABP44847 | 23 | 253 | 2      | 1024   |
| вгу                | ABP45400 | 23 | 251 | Ņ      | 1026   |
| aci                | AAG63639 | 22 | 304 |        | 1027   |
| n BLy              | ABP45531 | 23 | 251 | N      | 1027   |
| BLy:               | ABP46081 | 23 | 247 | 2      | 1027   |
| BLy:               | ABP44972 | 23 | 254 | 2      | 1027.5 |
| _                  | ABB06275 | 23 | 614 | 62.8   | 1028.5 |
| BLy:               | ABP45616 | 23 | 252 | N      | 1030.5 |
| BLy:               | ABP45298 | 23 | 251 | 2      | 1031   |
| Amino acid sequenc | AAG63634 | 22 | 304 | w<br>• | 1033   |
| BLyS               | ABP45409 | 23 | 250 | w      | 1035.5 |
| BLys b             | ABP44970 | 23 | 254 | ω<br>· | 1045.5 |
| BLyS               | ABP45351 | 23 | 252 | ũ      | 1045.5 |
| BLyS               | ABP45450 | 23 | 250 | ω<br>· | 1046.5 |
| BLyS               | ABP44828 | 23 | 256 | 4      | 1048.5 |
| BLyS               | ABP45447 | 23 | 260 | 4      | 1050.5 |
| BLyS               | ABP45830 | 23 | 258 | 4      | 1053.5 |
| BLyS               | ABP45942 | 23 | 247 | 4      | 1063   |
| 5                  | ABP45879 | 23 | 248 | 5      | 1064.5 |
| n BLyS             | ABP45958 | 23 | 243 | ū      | 1071   |
| rnalis             | AAY58235 | 21 | 246 | ÿ      | 1075.5 |
| n BLys bind        | ABP45190 | 23 | 252 | ō      | 1087.5 |
| n BLys bindin      | ABP44977 | 23 | 252 | Ġ      | 1089.5 |
| Human BLyS binding | ABP45508 | 23 | 252 | 7      | 1108.5 |

## ALIGNMENTS

TNF cytokine 09-FEB-1998; 15-MAY-1997; Homo sapiens. Single chain Apo-2 antibody 24C4. (GETH ) GENENTECH INC. AAW83324 standard; Protein; Human; Apo-2; receptor; apoptosis; neurodegenerative disease; cancer; tumour necrosis factor; TNF; tumour necrosis factor receptor; TNFR; Ashkenazi AJ, (first entry) 98US-0020746. 97US-0857216. 98WO-US09704 Chuntharapai A, 310 B Kim ζ,

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RESULT 2
ABB09605
ID ABB0
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Best Local S
Matches 310
   Bacteriophage
                                            Human; Apo-2;
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                                          tumour necrosis factor receptor; TNFR; apoptosis;
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                             cancer; antibody
                                                                      of single-chain Apo-2 antibody 24C4
                                                                                                      entry)
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100.0%; Pred. No. 3.;
tive 0; Mismatches
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1.7e-103;
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ABG74386 standard;

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                                                                                                                                                                                                                                                                                                                                                                                                                                              family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-21). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer, to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a single-chain Apo-2 antibody, decaded, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acids encoding an Apo-2 ligand, stimulating apoptosis in cancer cells, thus treatment of cancer, or in enhancing immune
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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09-FEB-1998;
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                                                                                                                                                                                     QMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGGGGSGGGGGGGGGGGSQSVLTQPP
                                                                                                                            SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                                                                                                               CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                                                                                                                                                                                                                                              CAASGEIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                          ISEEDLNGAA
                                                                    SGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHHGAAEQKL
                                                                                                              SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                                                       QMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGGGGGGGGGGGGGGGSQSVLTQPP
                                                     SGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHGAAEQKL
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98US-074119P
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                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                              Score 1638; DB 23; Pred. No. 3.7e-103; ; Mismatches 0;
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                                                                                                                                                                                                                                                                                             Query Match
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Matches 310
                                                                                                                                                                                                                                                                                                                                                                     The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays when labelled with, for instance, radioiodine, enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a diagnostic for tissue-specific typing. This is the amino acid sequence of the single chain antibody fragment (svFv) 24C4 used in the preparation of anti-apo-2 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Apo-2
apoptosis
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09-FEB-1998;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, or in generating antibodies against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                                                                                                                                                 Sequence
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310; Conserv
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ISEEDLNGAA
                                                                                                    SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                                     QMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGGGGSGGGGGGGGGGGSQSVLTQPP
                                                   SGTSASLAITGLQAEDEADYYCQSYDSSLRGSYFGGGTKVTVLGAAAHHHHHHGAAEQKL 300
                                                                                        SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                        QMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGGGGSGGGGGGGGGGSQSVLTQPP
                                      SGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHGAAEQKL
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98US-074119P.
98US-0079029.
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                                                                                                                                                                                                                                                                                             Score 1638; DB 24;
Pred. No. 3.7e-103;
; Mismatches 0;
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RESULT 4
AAW83322
                                                                                                                                The present invention describes human Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. CC Apo-2 is believed to be a new tumour necrosis factor (TWF) receptor CC (TWFR). TWF cytokines can induce apoptosis, thought to be initiated by binding to TWFRs, and Apo-2 triggered caspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat CC therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope trag polypeptide allow Apo-2 detection and purification using anti-tag comprisition approached to produce antibodies which can be combined CC with a (particularly pharmaceutically acceptable) carrier in compositions cor used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially Single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block cexcessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 cexpression in cells/tissues and in Apo-2 antibody, designated 16E2.
Query Match
Best Local S
Matches 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and partitional to increase or decrease apoptosis
                                                                                             Sequence
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15-MAY-1997;
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245; Conser
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75.2%; llarity 78.0%; Conservative 2
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is factor;
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97US-0857216.
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  20;
Score 1231.5; DB 2
Pred. No. 1.1e-75;
0; Mismatches 40;
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RRESULT 5
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                                                                      16E2, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cance to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and i affinity purification of Apo-2 from recombinant cell culture or nature
                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding an Apo-2 ligand, useful for activating stimulating apoptosis in cancer cells, thus especially useful in 1 treatment of cancer, or in enhancing immune-mediated cell death .
                                                                                                                                                                                                                                                                                                                                The present sequence represents a single-chain Apo-2 antibody,
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09-FEB-1998;
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DB; ABL41733.
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98US-074119P.
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Sequence

309

B

The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating

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RESULT 6
ABG74384
ID ABG77
XX ABG7
XX ABG7
XX ABG7
XX APO-
KW APO-
PR 09-I
PR 114-I
XX 15-I
PR 14-I
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Best Local S
Matches 245
                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1997;
09-FEB-1998;
14-MAY-1998;
                                                                                                                                                        New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, quantitative diagnostic assays, or in generating antibodies again Apo-2 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Apo-2; tumour necrosis factor family; TNFR; gen apoptosis; tissue-specific typing; affinity pur competitive-type receptor binding assay; mouse;
                                                                                                                                                                                                                                                                      WPI; 2003-198287/19.
N-PSDB; ABX16407.
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                                                                                                                Example 14;
                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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                                                                                                                                                                                                                                                                                                                                       Ashkenazi
                                                                                                              Fig 16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                              98US-0079029
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98US-074119P.
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                                                                                                              64pp; English.
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78.0%;
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Pred. No. 1.1
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AC AAW8
AC AAW8
AC Sing
XX Sing
XX Huma
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Human Apo-2 polypeptide inducing apoptosis - useful to treat conditions linked with decreased apoptosis e.g. cancer, and pantibodies to increase or decrease apoptosis
                                                                                                                                                                        Adams
                                                                                                                                                                                                                                                                 09-FEB-1998;
15-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                     W09851793-A1
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                                                                                                                                                                                                                                                                                                                                      14-MAY-1998;
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                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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                                                                                                1999-045228/04
DB; AAV72533.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QMNSLRAEDTAVYYCAR----DRGYYYMDVWGKGTTVTVSSGGGGSGGGGGGGGGGGGSQSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QMNSLRAEDTAVYYCAKILGAGRGWYF-DLWGKGTTVTVSSGGGGSGGGGGGGGGGS-SEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF
                                                                                                                                                                Ashkenazi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      309 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor; is factor;
                                                                                                                                                                                                                                                                 98US-0020746
97US-0857216
                                                                                                                                                                                                                                                                                                                                      98WO-US09704
                                                                                                                                                                     ΑJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            75.2%;
78.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 apoptosis; neurodegenerative disease;
TNF; tumour necrosis factor receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             309
                                                                                                                                                                   Chuntharapai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cancer;
TNFR;
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binding to TNFRs, and Apo-2 triggered casspase-dependent apoptosis. It can be used to identify agents activating Apo-2, useful to treat mammalian cancer cells, and to produce Apo-2 chimeras useful therapeutically (e.g. those containing immunoglobulin sequences can be inhibit apoptosis) or diagnostically (e.g. those comprising an epitope tag polypeptide allow Apo-2 detection and purification using anti-tag antibodies). It can be used to produce antibodies which can be combined with a (particularly pharmaceutically acceptable) carrier in compositions or used to produce dimeric molecules (especially homodimeric molecules comprising first and second Apo-2 antibodies). Agonistic (especially single-chain) antibodies can be administered to induce apoptosis in mammalian cancer cells, and antagonistic antibodies used to block excessive apoptosis (e.g. in neurodegenerative diseases). Apo-2 antibodies may also be used diagnostically e.g. to detect Apo-2 expression in cells/tissues and in Apo-2 antibody, designated 20E6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes human Apo-2. Apo-2 can be used therapeutically to induce apoptosis in mammalian cells, and so is useful to treat conditions associated with decreased apoptosis e.g. cancer. Apo-2 is believed to be a new tumour necrosis factor (TNF) receptor (TNFR). TNF cytokines can induce apoptosis, thought to be initiated by
Sequence
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312 AA;
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Query Match
Best Local S
Matches 247
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                                                    CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL 120
                                                                                                                                                                                                                                                                                     MTMITPSEGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGVVQPGRSLRLS
                                                                                                                           QSYLTQPPSYSGAPGQRYTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV
                                                                                                                                                                QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGGGGGGGGGGG
                                                                                                                                                                              QMNSLRAEDTAVYYCARD-----RGYYYMDVWGKGTTVTVSSGGGGSGGGGGGGGS 172
HGAAEQKLISEEDLNGAA 310
                                                                                                                                                                                                                     CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                                        MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAGVQLVESGGGLVQPGGSLRLS
                                                                                                          -SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                           75.2%; Score 1231; 77.7%; Pred. No. 1.
                                                                                                                                                                                                                                                                                                                              15;
                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                           DB 2
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ABB09604 standard; Protein; 312 A

ABB09604;

29-MAY-2002 (first entry)

Amino acid sequence of single-chain Apo-2 antibody 20E6

RESULT 8
ABB09AB0
XX | ABB0
XX | ABB0
XX | ABB0
XX | ABB0
XX | Amin
XX | Iuma
KW | Huma
KW | Casp
XX | Casp
XX | VS63
XX | US63 caspase; uman; Apo-2; apoptosis; tumour necrosis factor receptor; TNFR; apoptosis; tosis; cancer; antibody.

Bacteriophage

US6342369-B1

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RESULT 9
ABG74385
ID ABG7
XX
AC ABG7
XC ABG7
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DT 11-8
XX
DE Sing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence represents a single-chain Apo-2 antibody, designate 2026, which is isolated from a phage library. It is believed that Apo-2 is a member of the tumour necrosis factor receptor (TNFR) family. Apo-2 polypeptide is capable of triggering caspase-dependent apoptosis and activating nuclear factor-kappa B. A soluble extracellular domain of Apo-2 binds Apo-2 ligand (Apo-2L). Apo-2 antibodies may be used to activate or stimulate apoptosis in cancer cells. They are therefore especially useful in the treatment of cancer to enhance immune-mediated cell death in cells expressing Apo-2, to detect expression of Apo-2 in specific cells, tissues or serum, and in affinity purification of Apo-2 from recombinant cell culture or natural sources.
     Single chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acids encoding an Apo-2 ligand, useful for activating stimulating apoptosis in cancer cells, thus especially useful in treatment of cancer, or in enhancing immune-mediated cell death
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-MAY-1997;
09-FEB-1998;
                                                         11-APR-2003
                                                                                                             ABG74385;
                                                                                                                                                                ABG74385 standard;
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)B; ABL41734.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QMNSLRAEDTAVYYCARD------RGYYYMDVWGKGTTVTVSSGGGSGGGGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGVVQPGRSLRLS
                                                                                                                                                                                                                                                                                                                      HGAAEQKLISEEDLNGAA
                                                                                                                                                                                                                                                                                                                                                                                                   -SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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antibody (scFv) fragment
                                                   (first entry)
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98US-074119P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.28;
77.78;
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Pred. No. 1.2e
15; Mismatches
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L.2e-75;
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Query Match
Best Local :
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09-FEB-1998;
14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a novel isolated Apo-2 polypeptide. The Apo-2 polypeptide is useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, in quantitative diagnostic assays, as a control against samples containing unknown quantities of Apo-2, in generating antibodies, in affinity purification techniques, and in competitive-type receptor binding assays when labelled with, for instance, radioiodine, enzymes, or fluorophores. Nucleic acids encoding Apo-2 may be used as a diagnostic for tissue-specific typing. This is the amino acid sequence of the single chain antibody fragment (svFv) 20E6 used in the preparation of anti-apo-2 antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Apo-2 polypeptides and polynucleotides, useful for inducing apoptosis in mammalian cells, in vivo or ex vivo gene therapy, quantitative diagnostic assays, or in generating antibodies aga Apo-2
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                                                    HGAAEQKLISEEDLNGAA
                                                                                                                                                             QSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV
                                                                                                                                                                                                                                                                                                      CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                                                                                           CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                                                                                                                                        -SELTQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGI
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98US-074119P.
98US-0079029.
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                                                                                         Query Match
Best Local S
Matches 215
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                                                                                                                                            Sequence
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17-OCT-2000;
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                                                                                                                                    B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
administered to treat diseases associated with aberrant BLyS expre and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 repr
                                                                                                                                                                                                                                                                                                                                                                                                   This invention
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21-MAR-2001;
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B cell differentiation;
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Best Local S
Matches 211
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16-MAR-2001;
21-MAR-2001;
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of t
                                                                                                                                                                                                                                                                                                                   BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                 Antibodies against B Lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders -
                                                                                                           (HUMA-)
                                                                                                                                                                                                                                                                                                        antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunoc systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                       ABP45190;
            Claim
                                                                  WPI; 2002-114799/15
                                                                                                                                                                                                                                 10-JAN-2002
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                 common variable
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                                                                                                                                             25-MAY-2001;
                                                                                                                                                                                      16-JUN-2000;
                                                                                                                                                                                                            15-JUN-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    e antibodies and the invention.
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                                                                                                           HUMAN GENOME SCI INC
CAMBRIDGE ANTIBODY TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADSVKGRFTVSRDNSKNTLYLOMNSLRAEDTAVYYCARSHYDILTGLNYWYFDLWGRGTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR-----GYYYMDVWGKGTT
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                                                                                       Barash
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                                                                                                                                         2000US-212210P.
2000US-240816P.
2001US-276248P.
2001US-277379P.
2001US-293499P.
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                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
          1835-1836; 3148pp;
                                                                                                                                                                                                                                                                                                immunodeficiency; acquired immunodeficiency syndrome
                                                                                      sc,
                                                                                                            ANTIBODY TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                           SCFV SEQ ID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody;
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                                                                                                                           Region
                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Internalising anti-c-erbB-2 receptor antibody scFv F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-MAR-2000
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|||||::|||
1 VFGGGTQLTVL 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                            c-erbB-2 receptor; marker; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          252
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157..170
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  186..192
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                                                   /note=
                                                                                                                                                      note=
                                                                                                                                                                                                                                                                                                                                                                                                                 tumour-specific;
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84.1%;
                                                                                                                                                      "VH-CDR2"
                                                                                                                                                                                                       "Heavy chain determining
                                                                                                      "VH-CDR3
                     "Light chain variable region (VL) complementarity determining region 1 (CDR1)"
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internalisation;
                                                                                                                                                                                                       variable region (VH) complementarity
region 1 (CDR1)"
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                                                                                                                                                                                                                                                                                                                                                                                                              non-immunogenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cc may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin;
cc radionuclides; ligands such as growth factors; therapeutic agents such
cc as vinblastine, vindesine or melphalan; ribozymes; or antisense
cc molecules. The antibodies may also be used for in vivo or in vitro
cc detection and/or quantitation of the c-erb-2 receptor and thus diagnosis
cc and/or localisation of cancers characterised by expression of c-erb-2.
cc Although antibodies have previously been used to target tumour cells,
cc their success has been limited. The utility of prior art antibodies has
cc been hampered by the paucity of tumour specific antibodies, antibody
cc immunogenicity, low binding affinity, and poor tumour penetration.
cc tumour specific human antibodies were available. However, the production
cc tumour specific human antibodies were available. However, the production
cc of human monoclonal antibodies using conventional hybridoma technology
cc has proven difficult. Also, most of the antibodies produced react with
cn antipoles that are also common to non-malignant cells, which makes them
cn unsuffable for use as tumour-targetting molecules may antibodies them
                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents an internalising humanised antibody, scFv F5, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/neu oncogene. The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that is bound by F5 antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor is a marker protein which is overexpressed by 30-50% of breast carcinomas and other adenocarcinomas, and thus provides a useful cell surface marker for specifically targetting tumour cells. The antibodies of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            are used as tumour targetting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 81; 85pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel internalizing antibodies used
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12-FEB-1999;
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                                                                            This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, aftirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be associated with aberrant talseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CUD) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim
     Sequence
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systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
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Query Match

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17-OCT-2000;
16-MAR-2001;
21-MAR-2001;
25-MAY-2001;
                                          This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TMF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have
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  cytostatic, in antirheumatic
                                                                                                                                                               Claim
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CAMBRIDGE AND
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; 2001US-276248P.
; 2001US-277379P.
; 2001US-293499P.
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ic and antiAIDS act
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 inhibit the expression and activity of BLyS: The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and
                                                                                                                                                                                                                                                                                                                                                                                       diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method
                                                                                                                                                                                                                                                                                                                                                 Sequence
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               VFGGGTKVTVLG
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                                                                                                                                            VTVSSGGGGSGGGGGGGGSQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQ
                                                                                                                                                                         ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR---YYYHSSGSDAFDIWGQGTL
                                                                                                                                                                                       ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYYY-----
VFGGGTKLTVLG
                                                      LPGAAPQLLIYNNNQRPSGVPDRFSGSKSGTSASLAISGLQSEDEADYYCAAWDDSLNGW
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Search co completed: September ne : 53,9441 secs 22, 2003, 15:18:46

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Listing first 45 summaries
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1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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1638
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/cgn2_6/ptodata/1/1aa/BCTUS_COMB.pep:*
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-11
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GENERAL INFORMATION:
                                                                                                                           Query Match
Best Local Similarity
Matches 310; Conserv
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MEDIUM TYPE: 3.5 inch, 1.44 mb floppy di
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
NAME: MAISCHAUG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: 91101R2
TELEPHONE: 650/225-5116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Adams, Camilia W. APPLICANT: Ashkenazi, Avi J. APPLICANT: Chuntharapai, Anan APPLICANT: Kim, Kyung J. TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
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STATE: California
COUNTRY: USA
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CITY: S
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US-09-184-082-16
US-09-1184-082-16
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US-10-039-785-45
US-09-485-7378-2
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Pred. No. 5.2e-120;
0; Mismatches 0;
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Minimum DB: Maximum DB:

Scoring table: Sequence: Title: Perfect score: OM protein -

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APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuntharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                   CLASSIFICATION:
CLASSIFICATION:
ATTORNEY AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                       TYPE: Amino Acid
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                                                                                                                                      Local
                                                                                                                                                                                           TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                         245;
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                                                                               1 MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGVVQPGRSLRLS
                                                                                                                                      Similarity
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California
                          CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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                                                                MTMITPSFGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAEVQLVQSGGGVERPGGSLRLS
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                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                   inch, 1.44 Mb floppy disk
                                                                                                                     75.2%; Score 1231.5; DB 4; 78.0%; Pred. No. 2.1e-88; tive 20; Mismatches 40;
                                                                                                                                                                                                                                                                                                                                                                                  US/09/079,029
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                                                                                                                        Indels
                                                                                                                                              Length
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US-09-079-029-10
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Patent No.
                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIOM TYPE: 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DO
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 94080
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                         121 QMNSLRAEDTAVYYCARD------RGYYYMDVWGKGTTVTVSSGGGGSGGGGSGGGG 172
                                                                                                                                                              247;
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                                                                61 CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
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CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
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1 DNA Way
                                                                                                                                                               Conservative
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Ashkenazi, Avi J.
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                                                                                                                                                                                                                                  Linear
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/ 77.7%; Pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1.44 Mb floppy disk
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                                                                                                                                                                          Score 1231; DB 4;
Pred. No. 2.4e-88;
                                                                                                                                                               Mismatches
                                                                                                                                                                                          DB 4;
                                                                                                                                                               42;
                                                                                                                                                                                      Length 312;
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PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 3
SEQ ID NO 53
LENGTH: 334
TYPE: PRT
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                                                                                                                                   RESULT 5
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US-09-646-028-53
                                                                      Sequence 55, Applica Patent No. 6562347 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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Patent No. 656234
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APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSIFILE REFERENCE: 14014.0316/P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: US/09/646,028
CURRENT FILING DATE: 2000-09-12
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APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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                                                                                                     Application US/09646028
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               FUSION
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               PROTEINS
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               AS
               CANCER VACCINES
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SEQ ID NO 51
LENGTH: 348
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SEQ | ID NO 55
LENGTH: 339
                                                               Matches
                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No. 6562347
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                                                                                                                                                                                                                                                              APPLICANT: Kwak, Larry
APPLICANT: Biragyn, Arya
TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
FILE REFERENCE: 14014.0316/P
CURRENT APPLICATION NUMBER: 09/646,028
CURRENT FILING DATE: 2000-09-12
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR APPLICATION NUMBER: 60/077,745
PRIOR FILING DATE: 1998-03-12
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CURRENT FILING DATE: 2000-09-12
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                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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                                                               190;
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                 40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WYQKFPETAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYYCQCNDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TVTVSS-GGGGSGGGGGGGGG--GSQSVLTQPPSVSGAPCQRVTISCTGRSSNIGAGHDVH 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGGNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDR-GYYYMDVWGKGT
 EVQLLESGGGLVQSGGSLRLSCVASGLTFSSSAITWVRQAPGKGLEWVSGISFSGDTTYY 153
                                                                                                                                                                                                                                     FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVTVSSRGGGGGGGGGGGGGGGSGSQSVLTQPPSVSAAPGQRVTISCTGSRSNIGAGYDVN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SGDTTYYADSVKGRFSASRDNSKNTVYLQMNNLRPNDTAVYFCANNQTGNFCLDNWGQGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/09646028
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                                                               Conservative
                                                                                                                                                                                                                                     for Windows Version 3.0
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                                                                                                                                        Description
                                                                            60.0%;
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                                                             Score 983.5; DB 4;
Pred. No. 4.8e-69;
5; Mismatches 36;
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                                                                                                                                        of.
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                                                                                                                                        artificial sequence:/note-synthetic
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                                                               Indels
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                                                            7;
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                                                                                    ; NAME/KEY: SITE
; LOCATION: (271)...(280)
; OTHER INFORMATION: myc
US-09-184-658-40
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US-09-184-658-40
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                                      Matches
                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/184,658
CURRENT FILING DATE: 1998-11-02
EARLIER APPLICATION NUMBER: 60/065,423
EARLIER FILING DATE: 1997-11-13
NUMBER OF SEQ ID NOS: 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Otterness, Ivan G.
APPLICANT: Mezes, Peter S.
APPLICANT: Downs, James T.
APPLICANT: Johnson, Kimberly S.
TITLE OF INVENTION: Assays for Measur
TITLE OF INVENTION: Biological Media
FILE REFERENCE: PC9946-A
                                                                                                                                                                                                                                                                                                                                               NAME/KEY: SIGNAL
LOCATION: (1)..(22)
OTHER INFORMATION: POTHER INFORMATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                NAME/KEY: SITE
LOCATION: (262)..(267)
OTHER INFORMATION: His
                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY: DOMAIN
LOCATION: (138)..
                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
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OTHER INFORMATION: 15
                                                                                                                                                                                                                                                                                                           NAME/KEY: DOMAIN
LOCATION: (23)..(137)
                                                                                                                                       FEATURE:
                                                                                                                                                                                                LOCATION: (153)..(258)
OTHER INFORMATION: 9A4
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                                                                                                                                                                                                                          NAME/KEY: DOMAIN
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                                      181;
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5. 6030792
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TAPKVLIYSNNNRPSGVPDRFSGSKSGTSASLAITGLQLEDEGTYYCQCNDDSLSGWLFG
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                                      Conservative
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likely the initiator met
                                                                                                                                                                                                                                                                                                                                                                                                                      Description of Artificial Sequence: 9A4 scFv VH
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                                               Score 924.5; DB 3; Pred. No. 1.5e-64;
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                                      Mismatches
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                                    Indels
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                                    Gaps
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 Sequence 53, Application Patent No. 6538938
                                                                                                                                                                                                                                                                                                                        Matches
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; OTHER INFORMATION: Anti-homogalacturonan specific antibodies fro OTHER INFORMATION: phage display library known as the Synthetic; OTHER INFORMATION: Library (#1) from the Centre for Protein OTHER INFORMATION: Engineering, MRC Centre, Cambridge, UK. US-09-260-527-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        us-09-260-527-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/260,527A CURRENT FILING DATE: 1999-02-26 . NUMBER OF SEQ ID NOS: 7 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Applic
Patent No. 6228599
                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Knox, J.P.
APPLICANT: Wilkelsen, J.D.
APPLICANT: Willatts, W. G.
TITLE OF INVENTION: ANTIBODY
FILE REFERENCE: DYOULS 001AUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: UNKNOWN FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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 250
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                                                                                                                                                                                                                                                                                                33 AAQPAMAQVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGI--
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                        HVVFGGGTKLTVLGA--
                                                                                    QQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLR
                                GSVFGGGTKVTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 310
                                                                  QQKPGQAPVLVIYGKNNRPSGIPDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGN
                                                                                                                                         TLVTVSRGGGGGGGGGGGGGG-SELTQDPAVSVALGQTVRITCQGDSLR---SYYASWY
                                                                                                                                                                         TTVTVSSGGGGSGGGGGGGGSQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QAPGKGLKWMGWINTETGEPTYADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCAR
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                                                                                                                                                                                                                                                                                                                                                   Conservative
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69.3%;
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                                                                                                                                                                                                                                                                                                                                                                   Score 908.5; DB 3 Pred. No. 2.5e-63;
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 -AAEQKLISEEDLNGAA
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RESULT 10
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                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                             Sequence 76, Application US/08918148A Patent No. 6342220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. SEQ ID NO 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
               APPLICANT: Carter, Paul J.
APPLICANT: Fendly, Brian M.
APPLICANT: Gurney, Austin L.
TITLE OF INVENTION: Agonist Antibodies
FILE REFERENCE: P0979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                          APPLICANT: Adams, Camellia APPLICANT: W.
CURRENT APPLICATION NUMBER: US/08/918,148A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
TITLE OF INVENTION: Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PF550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OR APPLICATION NUMBER: 60/331,310
OR FILLING DATE: 2001-11-14
OR APPLICATION NUMBER: 60/331,044
OR FILLING DATE: 2001-11-07
OR APPLICATION NUMBER: 60/327,364
OR FILLING DATE: 2001-10-09
OR FILLING DATE: 2001-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 2002-04-05
APPLICATION NUMBER: 60/341,237
FILING DATE: 2001-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 60/294,981 FILING DATE: 2001-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/323,807 FILING DATE: 2001-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/309,176 FILING DATE: 2001-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGY-------YYMDVWGKGTT 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180;
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                                                                                                                                                                                                                                                                          WVFGGGTKVTVLG
                                                                                                                                                                                                                                                                                           SVFGGGTKVTVLG 284
                                                                                                                                                                                                                                                                                                                                              QRPGQSPVLVIYQDNKRPSGIPERFSGSNSGNTATLKISGTQAMDEADYYCLAWDSS-AD
                                                                                                                                                                                                                                                                                                                                                                              QLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRG 271
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPSSGGGSGGGGSAQSVLTQPPSVSVSPGQAARITCSG--DKLGDKY-ASWYQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAREPSFQQWGHYSYGMDVWGQGTM 120
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71.1%;
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Pred. No. 4.1e-63;
24; Mismatches 37
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RESULT 11
US-08-665-202-5
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Best Local S
Matches 178
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NUMBER OF SEQ ID NOS: 79
SEQ | ID NO 76
LENGTH: 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5, Application US/08665202 Patent No. 5977322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
INFORMATION FOR SEQ ID NO:
                                             REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
                                                                                                                  APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995
ATTORNEY/AGENT INCRMATION:
                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 941
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/665,202 FILING DATE: 13-JUN-1996
                               TELEPHONE:
                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                     NAME: Hunter, Tom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: San Francisco
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178; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MAEVQLVQSGGGVVQPGGSLSLSCAVSGITLRTYGMHWVRQAPGKGLEWVAGISFDGRSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APKLLIYKASSLASGAPSRFSGSGSGTDFTLTISSLQPDDFATYYCQQY--SNYPLTFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGGSGGGGGGGSDIQMTQSPSTLSASIGDRVTITC--RASE-GIYHWLAWYQQKPGK 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
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                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
               (415) 576-0200
(415) 576-0200
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                                                                                                                                                                                                              US 60/000,238
                                                                     02307E-061410
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US-09-315-574-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 170;
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Best Local S
ATTOMMANDE: HUNTER, TOM
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 023
TELECOMMUNICATION INFORMATION:
(415) 576-0200
                                                                                                                                                                             CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Marks, James ...
APPLICANT: Schier, Robert
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies
mrmr.r OF INVENTION: Tumor Antigens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 258 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN PC-BCASE #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                APPLICATION NUMBER: US 60/000,250 FILING DATE: 15-JUN-1995 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
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                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                    APPLICATION NUMBER: US 0 FILING DATE: 13-JUN-1996
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US, FILING DATE: 20-MAY-99
                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111-4106
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                                                                                                                                                                                                                                                                                                                                                                                                                                        San Francisco
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDS 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAR-DRGY------YMDVW 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GKGTTVTVSSGGGGSGGGGSGGGGSQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDV 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YSPSFQGQVTISVDKSVSTAYLQWSSLKPSDSAVYFCARHDVGYCSSSNCAKWPEYFQHW
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                                                                                                                                                                                                                                                                                                                                                                                                                        California
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Four Embarcadero Center,
                                                                                                                                                                                                                                                                                                                                                                                                            USA
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                                                                                                                   US 08/665,202
                                                                                                                                                                                                                                                                                US/09/315,574
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                                       02307E-061411
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Pred. No. 9.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       Siebert & Hsue P.C.
er, Suite 1100
                                                                                                                                                                                                                                                                                                            Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
.8e-59;
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                                                                                                                     ; NAME/KEY: PEPTIDE
; LOCATION: (177)..(279)
; OTHER INFORMATION: Identification Method: P
US-09-486-814A-2
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APPLICANT: TOHDOH, Naoki
TITLE OF INVENTION: SINGLE-CHAIN ANTIBODY AGAINST HEPATITIS
TITLE OF INVENTION: PROTEIN, GENE THEREOF, AND THERAPEUTIC
TITLE OF INVENTION: HEPATITIS B CONTAINING THESE
FILE REFERENCE: 0020-4682P
CURRENT APPLICATION NUMBER: US/09/486,814A
CURRENT APPLICATION NUMBER: US/09/486,814A
CURRENT FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 14
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2, Application US/09486814A Patent No. 6562599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: YAMAMOTO, Masato APPLICANT: HAYASHI, No. 656259910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                      LENGTH: 297
TYPE: PRT
                                                                                                                                                                                             LOCATION: (1)..(145)
OTHER INFORMATION: Identification
                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                            NAME/KEY: PEPTIDE
                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                      ORGANISM: Mus sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 258 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Match 51.8%; Score 849; DB 4; Local Similarity 65.4%; Pred. No. 9.8e-59;
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Similarity
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                                                            Conservative
                                                                                                                                                                                                                                                          strain: Balb/c,
                                                                           51.8%;
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                                                                           Score 848.5; DB 4; Pred. No. 1.3e-58;
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                                                           Mismatches
                                                                                                                                                                                                Method:
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RESULT 14
US-09-553-498-8
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US-09-618-869-8
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Best Local S
Matches 173
                                             Sequence 8, Application US/09618869
Patent No. 6455279
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8, Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10
SEQ ID NO 8
LENGTH: 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Schwarz, Elisabeth
TITLE OF INVENTION: Process for the production of naturally folded and secreted prote
FILE REFERENCE: Case 20379
CURRENT APPLICATION NUMBER: US/09/553,498
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: EP99107412.1
PRIOR FILING DATE: 1999-04-26
                      APPLICANT:
 APPLICANT:
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No. 6309861
INFORMATION:
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Ambrosius, Dorthee
Rudolph, Rainer
Schaeffner, Joerg
Schwarz, Elisabeth
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                                                                                                                                                        GTKVTVLGAAAHHHHHHGAAEQKLISEEDLNGAA 310
                                                                                                                                                                                                                            GGGGSGGGSGGGSDIELTQSPAIMSASPGEKVTMTCSASSS----VRYMNWFQQKSGT
                                                                                                                                                                                                                                                      GGGGSGGGGGGGGSQSVLTQPPSV-SGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGT
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Schaeffner, Joerg
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US-09-618-869-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: PROCESS FOR THE PRODUCY
TITLE OF INVENTION: SECRETED PROTEINS BY CO
TITLE OF INVENTION: CHAPERONES
FILE REFERENCE: 20381
CURRENT APPLICATION NUMBER: US/09/618,869
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: EP99114811.5
PRIOR FILING DATE: 1999-07-29
                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER: Pate SOFTWARE: Pate ; SEQ | ID NO 8
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Best Local S
Matches 173
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completed: September ne : 19.3136 secs
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                                                                                                                               217 APKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGG
                                                                                                                                                                 231 GTKLELKRA---
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                                                                                                                                                                                                                                                                                                                                      Similarity 63.1
73; Conservative
                                                                     GTKVTVLGAAAHHHHHGAAEQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Ver. 2.1
                                                                                                            SPKRWIYDTSKLSSGVPARFSGSGSGTSYSLTISSMEAEDAATYYCQQWSSN--PLTFGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROCESS FOR THE PRODUCTION OF NATURALLY FOLDED SECRETED PROTEINS BY CO-SECRETION OF MOLECULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
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             15:16:02
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hes 51;
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1089.5
1087.5
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1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
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) /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
) /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
1 /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
2 /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
3 /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
4 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
5 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
5 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
7 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
7 /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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US-10-288-917-11

US-10-052-798-11

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US-10-052-798-10

US-10-052-798-10

US-09-880-748-1519

US-09-880-748-1201

US-09-880-748-1890

US-09-880-748-1890

US-09-880-748-1891

US-09-880-748-1891

US-09-880-748-1893

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1345.823 Million cell updates/sec
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                             Sequence 11, Appl
Sequence 9, Appli
Sequence 9, Appli
Sequence 10, Appli
Sequence 10, Appl
Sequence 1519, Appl
Sequence 1201, Appl
Sequence 1201, Appl
Sequence 1969, 
   1458,
839, F
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| 1004.5        | 1004.5          | 1005.5          | 1005.5       | 1005.5          | 1006.5          | 1008            | 1010.5   | 1012            | 1012.5          | 1015.5        | 1016            | 1018            | 1020            | 1021          | 1021           | 1021.5        | 1023          | 1023.5         | 1024          | 1026         | 1027          | 1027            | 1027.5        | 1030.5        | 1031            | 1035.5          | 1045.5   | 1045.5          | 1046.5     |
|---------------|-----------------|-----------------|--------------|-----------------|-----------------|-----------------|----------|-----------------|-----------------|---------------|-----------------|-----------------|-----------------|---------------|----------------|---------------|---------------|----------------|---------------|--------------|---------------|-----------------|---------------|---------------|-----------------|-----------------|----------|-----------------|------------|
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| 240           | 240             | 240             | 240          | 240             | 240             | 241             | 240      | 251             | 254             | 252           | 253             | 249             | 251             | 247           | 247            | 254           | 251           | 254            | 253           | 251          | 251           | 247             | 254           | 252           | 251             | 250             | 254      | 252             | 250        |
| 11            | 11              | 11              | 11           | 11              | 11              | H               | 11       | 11              | 11              | 11            | 11              | 11              | 11              | 11            | 11             | 11            | 11            | 11             | 11            | 11           | 11            | 11              | 11            | 11            | 11              | 11              | 11       | 11              | 11         |
| -09-880-748-2 | -09-880-748-201 | -09-880-748-204 | -880-748-202 | -09-880-748-200 | -09-880-748-190 | -09-880-748-205 | 80-748-2 | -09-880-748-131 | -09-880-748-113 | -09-880-748-9 | -09-880-748-120 | -09-880-748-195 | -09-880-748-133 | -09-880-748-1 | 48-189         | -09-880-748-E | -09-880-748-9 | -09-880-748-1  | -09-880-748-8 | -880-748-141 | -09-880-748-1 | -09-880-748-209 | -09-880-748-9 | -09-880-748-1 | -09-880-748-130 | -09-880-748-142 | 80-748-9 | -09-880-748-136 | 80-748-146 |
| equence       | equence         | equence         | ര            | equence         |                 |                 |          |                 |                 |               |                 |                 |                 |               | Sequence 1892, |               |               | Sequence 1759, |               |              |               | (U              | Sequence 983, | w             | equence         | Ø               | quence   | equence         | equence    |
| ,<br>Ap       | φ               | Αp              | ,<br>Ap      | ,<br>Ap         | Αp              | Αp              | Αp       | Αp              | Αp              | App           | Αp              | Αp              | Αp              | Αp            | Αp             | App           | App           | Ą              | App           | Αp           | Αp            | Αp              | App           | Αp            | Αþ              | Αp              | App      | Αp              | ,<br>Ab    |
|               |                 |                 |              |                 |                 |                 |          |                 |                 |               |                 |                 |                 |               |                |               |               |                |               |              |               |                 |               |               |                 |                 |          |                 |            |

ALIGNMENTS

WESULF 1
US-10-288-917-11
Sequence 11, Application US/10288917
Sequence 11, Application US/10288917
Sequence 11, Application US/20030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC. COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION NUMBER: US/10/288,917
FILING DATE: 06-NO. US20030148455A1-2002
APPLICATION NUMBER: 10/052798
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 09/079029
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.

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US-10-052-798-11
; Sequence 11, Application US/10052798
; Publication No. US20020150985A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; SEQUENCE DESCRIPTION: SEQ ID NO: 11: US-10-288-917-11
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                                              COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/052,798

FILING DATE: 02-No. US20020150985A1-2001

CLASSIFICATION: <UNKnown>

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                         Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
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                                                                                                                                                                                                                                                                                     ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                                                                                                                                   CITY: South San F
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: Amino Acid
                APPLICATION NUMBER: US/09/079,029 FILING DATE: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 650/952-9881
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Kim, Kyung J.
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Pred. No. 8.4
0; Mismatches
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8.4e-106;
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US-10-288-917-9
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Best Local Similarity
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                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/288,917

FILING DATE: 06-No. US20030148455A1-2002

CLASSIFICATION: CUNknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/052798
FILING DATE: 02-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
Chuntharapai, Anan
                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 310 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSR
                                                                                                                                                                                                                               COUNTRY: USA
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STATE: California
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TELEFAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Marschang, Diane L. REGISTRATION NUMBER: 35,600
                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1101R2
                                                                                                                                                                                                                                                                                                        ADDRESSEE: Genentech,
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US-10-052-798-9
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                                                                                                                                                                                                                                                                                         Sequence 9, Application US/10052798
Publication No. US20020150985A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 245;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                   Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 15-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QMNSLRAEDTAVYYCAR----DRGYYYMDVWGKGTTVTVSSGGGSGGGGGGGGGGGSQSVL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGIPDRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL 120
                                                                                                                                CITY: South San Fr
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EQKLISEEDLNGAA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHGAA 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGVPDRF 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 09/079029
FILING DATE: 14 MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
                                                                                                               COUNTRY: USA
                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                                                     ADDRESSEE: Genentech, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                             94080
                                                                                                                                                                                                                                                                              Chuntharapai, Anan
                                                                                                                                                                    1 DNA Way
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78.0%;
                                                                                                                                                 Francisco
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Pred. No. 1e-77;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 12;
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US-10-288-917-10
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Publication No. US/0030148455A1
GENERAL INFORMATION:
APPLICANT: Adams, Camilia W.
Ashkenazi, Avi J.
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INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: Amino acids
TYPE: Amino acid
TYPE: Amino acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 650/225-5416
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ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                 TITLE OF INVENTION: Apo-2 Receptor NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
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                                                                                          CITY: South San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHHHGAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAASGFTFDDYGMSWVRQAPGKGLEWVSGINWNGGSTGYADSVKGRVTISRDNAKNSLYL
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FILING DATE: 02-No. US20020150985A1-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHHHGAA
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                                                                      ZIP: 94080
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                                                                                                                                                                                                                                       Kim, Kyung
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78.0%;
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Pred. No. 1e-77;
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                                                                                                                                                                Inc.
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Gaps

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RESULT 6
US-10-052-798-10
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                                                                                                                                                                                                                        Sequence 10, Application US/10052798 Publication No. US20020150985A1
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                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 10: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                    Kim, Kyung J.
TITLE OF INVENTION: Apo-2 Receptor
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MAISCHARP, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2D1C1
TELECOMMUNICATION INFORMATION:
TELEFAX: 650/225-5416
TELEFAX: 650/952-9881
                                                                                                                                                           APPLICANT: Adams, Camilia W. Ashkenazi, Avi J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE DESCRIPTION: SEQ ID NO: 10:
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FILING DATE: 02-NOV-2001
APPLICATION NUMBER: 09/079029
FILING DATE: 14-MAY-1998
APPLICATION NUMBER: 60/074119
FILING DATE: 09-FEB-1998
APPLICATION NUMBER: 60/046615
FILING DATE: 15-MAY-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MTMITPSEGAFFLEIFNVKKLLFAIPLVVPFYAAQPAMAQVQLVQSGGGVVQPGRSLRLS
                                                                                                                                                                                                                                                                                                                                                                HGAAEQKLISEEDLNGAA 310
                                                                                                                                                                                                                                                                                                                                                                                                                                            PDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQLPGTAPKLLIYDDSNRPSGV 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/10/288,917
EILING DATE: 06-No. US20030148455A1-2002
CLASSIFICATION: -(Unknown>
                                                                                                                                                                                                                                                                                                                                          HGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                   PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QMNSLRAEDTAVYYCARD-----RGYYYMDVWGKGTTVTVSSGGGGSGGGGSGGGS 172
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      STREET: 1 DI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SELTQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGI
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77.78;
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Pred. No. 1.1e-77
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                                                                                                                                                                             RESULT 7
US-09-880-748-1519
; Sequence 1519, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
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Best Local
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR PILING DATE: 2000-10-17
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MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
ANAME: MATSCHANG, Diane L.
REGISTRATION NUMBER: 35,6
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PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVKGRFTISRDNSKNTLYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDRFSGSSSGNTASLTITGAQAEDEADYYCNSRDSSGNHVVFGGGTKLTVLGAAAHHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                         PDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLGAAAHHHH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QMNSLRAEDTAVYYCARDLLKVKGSSSGWF--DPWGRGTTVTVSSGGGGSGGGSGGGGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAASGFTFSSYWMSWVRQAPGKGLEWVANIKQDGSEKYYVDSVKGRFTISRDNAKNSLYL
                                                                                                                                                                                                                                                                                                                        HGAAEQKLISEEDLNGAA 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -SELTQDPAVSVALGQTVRITCQGDSLR----SYYASWYQQKPGQAPVLVIYGKNNRPSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 312 amino acids TYPE: Amino Acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/10/052,798 FILING DATE: 02-No. US20020150985A1-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/09/079,029
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: WinPatin (Genentech)
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77.7%;
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Pred. No. 1.1e-77;
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PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR PLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1519
LENGTH: 252
TYPE: PRT
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                                                                                                     ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-988
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                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
                                                                                                                                              PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 988
LENGTH: 252
                                               Matches
                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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                                                                                                                                                                                                                                      APPLICATION NUMBER: 60/277,379 FILING DATE: 2001-03-21
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40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY :||||:|||:||| |:|| |:|| |:|| |:||
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83.4%;
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85.3%;
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                                          Score 1089.5; DB 11; Length 252;
Pred. No. 5.2e-68;
4; Mismatches 19; Indels 9;
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; ORGANISM: Homo sapiens
US-09-880-748-1201
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US-09-880-748-1201
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PRIOR FILING DATE: 2000-06-15
PRIOR PRIOR DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-16
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
JEQ ID NO 1201
LENGTH: 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
241
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                                                                               213 LPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGS
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 VEGGETQLTVL
                             VEGGGTKVTVL
                                                               LPGTAPKLLIFGNNNRPSGVPDRFSGSKSGTSASLAITGLQGEDEADYYCQSFDTSLGVR
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Pred. No. 7.1e.
14; Mismatches
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US-09-880-748-1890
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           PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR PELICATION NUMBER: 60/240,816
PRIOR FILLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/297,379
PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR FILING DATE: 2000-06-15
PRIOR PELICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                                                                                            Sequence 1890, Application US/09880748 Publication No. US20030059937A1
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically
FILE REFERENCE: PF523
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CURRENT FILING DATE: 2001-06-15
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NUMBER OF SEQ ID NOS: 3239
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Local Similarity 84.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WARE: Patentiń Ver.
FILING DATE:
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1890
                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2010-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1953
LENGTH: 247
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SEQ ID NO 1890
LENGTH: 248
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                          Local Similarity 84.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 VTVSSGGGGSGGGGGGGSQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVHWYQQ 212
                                100 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYYY------MDVWGKGTT 152
159 GGGSGGGGGGGGS-QSVLTQPPSVSGAPGQRVTTSCTGRSSNIGAGHDVHWYQQLPGTA
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Pred. No. 3.4e-66;
1; Mismatches 26
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US-09-880-748-1458
US-99-880-748-1458
; Sequence 1458, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
APPLICANT: RUBen et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind
; FILE REFERENCE: PF523
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US-09-880-748-1841
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Best Local S
Matches 207
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1841
LENGTH: 258
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PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind FILE REFERENCE: PF523
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CURRENT FILING DATE: 2001-06-15
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207; Conserv
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                                                                                                                                                                                                                                                                                                                    VHWYQQLPGTAPRLLIYGNSNRPSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYD 240
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80.2%; Pred. No. 1.6e-65;
rative 17; Mismatches 21
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                                                                                                                                                                          FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR FILING DATE: 2000-06-15

PRIOR PRILING DATE: 2000-10-17

PRIOR PPLICATION NUMBER: 60/276,248

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR PPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25

PRIOR FILING DATE: 2001-05-25
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US-09-880-748-839
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1458
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
                                                                      SOFTWARE: Pate
SEQ ID NO 839
LENGTH: 256
TYPE: PRT
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Best Local Similarity 78.5.
205; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1458
LENGTH: 260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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                                                                                                                                                              NUMBER OF SEQ ID NOS: 3239
                                                 ORGANISM: Homo sapiens
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                                                                                                                                        PatentIn Ver.
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Indels Length

17;

Gaps

4;

| Search co<br>Job time                          | Qy                       | Qу   | Оy   | Qу   | Qy<br>Db  | Query Match<br>Best Local :<br>Matches 20   |
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| Search completed: September 22, 2003, 15:36:25 | 269 LRGSVFGGGTKVTVLG 284 | 209 WYQQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSS 268 | 149 KGTTVTVSSGGGSGGGGSGGGSQSVLTQPPSVSGAPGQRVTISCTGRSSNIGAGHDVH 208 | 101 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYYYMDVWG 148 | 41 VQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYA 100 | Query Match 64.0%; Score 1048.5; DB 11; Length 256; Best Local Similarity 79.5%; Pred. No. 3.6e-65; Matches 205; Conservative 14; Mismatches 22; Indels 17; Gaps 3; |
| Job time : 35.2965 secs                        |                          |  |  |  |   |   |

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Listing first 45 summaries
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    protein search, using sw model

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1421.159 Million cell updates/s
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Copyright (c) 1993 - 2003
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chain Fv an
                         RESULT 2
$4.1374
$single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #t
C;Accession: $41374
C;Accession: $41374
R;Artsaenko, O; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C Species: Mus musculus (house mouse) c;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_ch C;Accession: A56446 R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A. J. Biol. Chem. 270, 7829-7835, 1995 A;Title: A high affinity digoxin-binding protein displayed A;Reference number: A56446; MUID:95229583; PMID:7713873 A;Accession: A56446 A;Status: preliminary
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A;Residues: 1-268 <TAN>
A;Cross references: GB:U20617
C;Keywords: heterotetramer; immunoglobulin
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55.2%; Pred. No. 2.16
tive 36; Mismatches
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                                 y 1994
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Result No.

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Query Match

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Minimum DB Maximum DB

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1: pir1:\*
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3: pir3:\*
4: pir4:\*

Sequence: Title: Perfect score:

US-10-052-798-11 1638

Scoring table:

BLOSUM62 Gapop 10.0 ,

283308 seqs,

OM protein

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RESULT 3
$48797

Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH6) - human (fragment)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Sep-1998 #text_change 23-Jul-1999
C;Accession: $26893
R;Mahmoudi, M; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A;Description: Molecular characterization of natural human anti-Sm autoantibodie:
A;Reference number: $48797
A;Accession: $48797
A;Accession: $48797
A;Accession: $48797
A;Accession: $1-128 cMAH>
A;Residues: 1-128 cMAH>
A;Cross-references: EMBL: 246379; NID: 9587147; PIDN:CAA86512.1; PID: 91340168
A;Cross-references: EMBL: 246379; NID: 9587147; PIDN:CAA86512.1; PID: 91340168
A;Cross-references: EMBL: 26379; NID: 9587147; PIDN:CAA86512.1; PID: 91340168
A;Accession: $26893
A;Accession: $26895; MUID: 93021117; PMID: 1404388
A;Reference number: $26885; MUID: 93021117; PMID: 1404388
A;Residues: 1-98 cMOM>
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A; Residues: 1-249 <ART>
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A; Status: preliminary
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                                                                                                                                                                                                                             40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
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                                                                                                                                                                                                     QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKGLEWVAVIWYDGSNKYY
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                                                                                                                                                                                                                                                                                                     Score 569; DB Pred. No. 1.4e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 619; DB 2;
Pred. No. 1.3e-34;
1; Mismatches 80
                                                                                                                                                                                                                                                                                                                             DB 2; Length 128, 4e-31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; 08
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p53 specific single-chain antibody Pab421 - human (Species: Homo sapiens (man) (C;Species: Homo sapiens (man) (C;Date: 15-May-1997 *sequence_revision 15-May-1997 *text_change 18-Jul-1997 (;Accession: JC5322 R;Jannot, C.B.; Hynes, N.E. Blochem. Biophys. Res. Commun. 230, 242-246, 1997 Blochem. Biophys. Res. Commun. 230, 242-246, 1997 A;Title: Characterization of scFv-421, a single-chain antibody targeted to A;Reference number: JC5322; MUID:97168950; PMID:9016757 A;Accession: JC5322; MUID:97168950; PMID:9016757 A;Accession: JC5322; MUID:97168950; PMID:9016757
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                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-233 < JAN>
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C; Superfamily: immunoglobulin V region; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Gene: GDB:IGH@; IGHDY1
A;Cross-references: GDB:
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A; Residues: 1-122 <SCH>
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Best Local Similarity
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Best Local :
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                   165 GGSGGGGSQSVLTQ-PPSVSGAPGQRVTISCTGRSSNIGAGHD-VHWYQQLPGTAPKLLI
                                                                                            105 GRETISRDNSKNTLYLOMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGGGGSGG 164
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                                                                                                                                                    45 QSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYYADSVK 104 :|| :|: || :|| :||: || :||: ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
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                                                                                                                                 ESGAELVRSGASVKLSCTTSGFNINDYYMHWVKKRPEQGLEWIGRIDPENGDADMTRSSG
RASGGGGSDIELTQSPASLAVSLGQRATISCRASKSVSTSGYSYMHWNQQKPGQPPRLLI
                                                                  VKATMTADTSSNTAYLQLSSLTSEDTAVYYC - - NAG - - - MDYWGQGTTVTVSSGGGGSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SS 157
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14q32.33-14q32.3
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                                                                                                                                                                                                    32; Mismatches
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                                                                                                                                                                                                                  Score 556; DB 2
Pred. No. 2e-30;
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Pred. No. 5.
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5.5e-31;
7;
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S31603

1g heavy chain V region - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 03-Mar-1994 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C;Accession: S31603
R;Culsinler, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelle, C.
submitted to the EMBL Data Library, June 1992
A;Description: Mechanisms that generate human immunoglobulin diversity operate 1
A;Reference number: S31585
A;Accession: S31603
A;Accession: S31603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38493
R;Marks, J.D.; Ouwehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Tsubmitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens A;Reference number: S38488
A;Accession: S38493
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                                                                                                                                                                                           A:Molecule type: mRNA
A:Residues: 1-132 <CUI>
A:Residues: 1-132 <CUI>
A:Cross-references: EMBL:Z14168; NID:g30999; PIDN:CAA78537.1; PID:g31000
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:30-113/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-123 <MAR>
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Best Local
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Best Local Similarity
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121 VSS 123
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                                                                                                                                            similarity 88.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSS 157
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                                                                                                                                            Score 545.5; DB 2
Pred. No. 5.5e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 555.5; DB 2
Pred. No. 1.1e-30;
                                                                                                                             Mismatches
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antibody light chain V region - human (fragment)
C; Species: Homo sapiens (man)
C; Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
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519666
19 heavy chain V region (VH3DJH4) - human
19 heavy chain V region (WH3DJH4) - human
19 heavy chain V region (Man)
19 C;Species: Homo sapiens (man)
19 C;Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: By-passing immunization. Human antibodies from V-gene A;Reference number: S19663; MUID:92085276; PMID:1748994 A;Accession: S19666
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A; Residues: 1-121 < MAR>
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C;Species: Homo sapiens (man)
C;Date: 02-Dec_1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
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R; Raaphorst, F.M.;
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3; Mismatches
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Pred. No. 9.4e-30;
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Pred. No. 6.2e-30;
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C;Accession: S51148
R;de Kruif, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, Januar
A;Description: Selection and application c
A;Reference number: S51147
A;Accession: S51148
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-112 <DBK>
A;Cross-references: EMBL:X83713
C;Superfamily: immunoglobulin homology <1
                          Ig heavy chain V region (M74) - human
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change
C; Accession: G36005
R; Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A; Title: Preferential utilization of conserved immunoglobulin
A; Reference number: A36005; MUID:90349571; PMID:2117273
A; Accession: G36005
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C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998
C;Accession: S70442
R;Culsinier, A.M.; Fumoux, F.; Fougereau, M.; Tonne
Mol. Immunol. 29, 1363-1373, 1992
A;Title: IgM kappa/lambda EBV human B cell clone: &
A;Reference number: S70442; MUID: 93024508; PMID: 138
A;Accession: S70442
A;Status: not compared with conceptual translation
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A; Residues: 1-140 <CUI>
C; Superfamily: immunoglobulin V
F; 34-117/Domain: immunoglobulin
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A;Status: F
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4BL Data Library, January 1995

10tion and application of human

S51147
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C;Species: Homo sapiens (man)
C;Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999
C;Accession: S31117
R;Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.
Eur. J. Immunol. 22, 247-251, 1992
A;Title: Restricted utilization of germ-line V(H)3 genes and short diverse t A;Reference number: S31104; MUID:92111633; PMID:1730252
A;Accession: S31117
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A; Cross-references: GB:M34031
C; Genetics:
A; Gene: GDB:IGH@; IGHDY1
A; Cross-references: GDB:11873
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C; Keywords: hete
F; 15-98/Domain:
Ig heavy chain V region - numan c;Species: Homo sapiens (man) C;Date: 03-Mar-1994 #sequence_revision 10 C;Accession: S31601 R;Cuisinier, A.M.; Gauthier, L.; Boubli, submitted to the EMBL Data Library June h;Description: Mechanisms that generate h
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C;Superfamily: immunoglobulin V region; immunoglobulin C;Keywords: heterotetramer; immunoglobulin E;15-98/Domain: immunoglobulin homology <IMM>
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A; Residues: 1-122 < RAA>
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Best Local
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Pred. No. 1.1e
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Score 539; DB 2;
Pred. No. 1.4e-29;
5; Mismatches 9
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               June 1992
                                                           10-Nov-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M.J.H.; van Tol, M.J.D.; Vossen, J.M.;
                             Fougereau, M.;
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comp

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F36005

Ig heavy chain V region (M49) - human
C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Dec-1998
C; Accession: F36005
R; Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A; Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene A; Reference number: A36005; MUID:90349571; PMID:2117273
A; Accession: F36005
A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-119 <SCH>
A; Cross-references: GBB:M34026
C; Genetics:
A; Gene: GDB:IGH@; IGHDY1
A; Cross-references: GDB:118731; OMIM:146910
A; Map position: 14q32.33-14q32.33
C; Superfamily: immunoglobulin v region; immunoglobulin homology
C; Meywords: heterotetramer; immunoglobulin homology
C; Mystation: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: S31585
A;Accession: S31601
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-130 <CUI>
A;Cross-references: EMBL:Z14192; NID:g31018; PIDN:CAA78561.1; PID:g31019
C;Keywords: heterotetramer; immunoglobulin homology
F;30-113/Domain: immunoglobulin homology <IMM>
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Search completed: September 22, Job time: 21.9774 secs
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120 WGQGTLVTVSS 130
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81.7%;
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Pred. No. 2e-29;
4; Mismatches
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| egrande (* 1851)<br>Poprinski skriver (* 1861) |   | •    |         | · · · · · · · · · · · · · · · · · · · | •  | ÷                                      |
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Sequence: Title: Perfect score:

US-10-052-798-11 1638

Scoring table:

BLOSUM62 Gapop 10.0 ,

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2 homo sapien
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                 LV1A_HUMAN
HV05_CARAU
LV1I_HUMAN
HV3D_HUMAN
HV3B_MOUSE
HV30_HUMAN
HV20_MOUSE
HV18_MOUSE
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HV3E_HUMAN
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HV16_MOUSE
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Best Local s
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SMART; SM00406; IGv; 1.

PROSITE; PS50835; IG_LIKE; 1

Immunoglobulin V region; Pyr

DOMAIN
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SEQUENCE
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                                                                                                                                                                                                                                                       GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
rd heavy chain V-III region CAM.
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                                                        40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
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                                                                                               QVELVESGGGVVZPGRSLRLSCAASGFTFSNYAMHWVRQPPGKGLEWVAVISYBGBBKYY
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122 AA;
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13668 MW; A42D0F17D252F1C2 CRC64;
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77.0%;
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HV35_MOUSE
HV25_MOUSE
HV22_MOUSE
HV40_MOUSE
LV2K_HUMAN
HV37_MOUSE
LV2D_HUMAN
HV02_CANFA
HV01_RAT
HV55_MOUSE
                                                                                                                                    Score 503; DB 1;
Pred. No. 4.4e-30;
2; Mismatches 12
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RESULT 3
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Matches 92
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InterPro; IPR007110; Ig-1ike.
InterPro; IPR003006; Ig_MIG.
InterPro; IPR0030596; Ig_W.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
Immunoglobulin V region; Pyrrolidone
DOMAIN

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IG-LIKE
IG-LIKE
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15-SEP-2003 (Re
Ig heavy chain
SEQUENCE, AND DISULFIDE BONDS.
MEDLINE-83289131; PubMed-6884994;
Schmidt W.E., Jung H.-D., Palm W., Hilschma
"Three-dimensional structure determination
                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
                                                                                                                                                                                                  HV3K_HUMAN STANDARD; PRT; 126 AA P01772; P01772; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 19 heavy chain V-III region KOL.
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HV3J_HUMAN
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Biochemistry 18:553-560(1979)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=79124695; PubMed=420800; Chiu Y.-Y.H., Lopez de Castro J.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: Contains 1 immunoglobulin-like domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
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; P01772; 2FB4.
                                                                                                                                                                                      sapiens (Human).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      40 QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
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121 AA;
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ain V-III region HIL.
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13566 MW;
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Pred. No. 9.
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SMART; SM00406; IGV;
PROSITE; PS50835; IG
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J. Mol. Biol. 141:369-
                                                                                                                                                                                              STRAND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS). MEDLINE-81072295; PubMed-7441755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure of crystallized monoclonal immunoglobulin IgG1 Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                           mmunoglobulin
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GO:0003823; F:antigen binding act
GO:0006955; P:immune response; NA
121
            152
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                                                                                     93;
                                                                                            Similarity
                                 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYYYM------DVWGKGT
                                                               QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
PVTVSS
             TVTVSS 157
                           ADSVKGRFTISRDNSKNTLFLQMDSLRPEDTGVYFCARDGGHGFCSSASCFGPDYWGQGT
                                                       QVQLVESGGGVVQPGRSLRLSCSSSGFIFSSYAMYWVRQAPGKGLEWVAIIWDDGSDQHY
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IPR003006; Ig_MHC.
IPR003596; Ig_v.
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                                                                                                                        Conservative
                                                                                                                 .26 AA;
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IG_LIKE;
                                                                                                                       13718 MW;
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73.8%;
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                                                                                   Score 482; DE Pred. No. 1.5e
                                                                                                                                                                                                                                                                                                              IG-LIKE.
PYRROLIDONE CARBOXYLIC ACID
                                                                                                                E4D71B52B16F8776 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    activity;
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RESULT 5
HV3H_HUMAN
ID HV3H_HUMAN
AC P01769;
DT 21-JUL-1986
DT 21-JUL-1986
DT 15-SEP-2003
DE Ig heavy cha
OS Homo sapiens
OC Eukaryota; b
OC Mammalia; Eu
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                                                               P01799;
P01799;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
To heavy chain V-III region GA.
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Ponsting1 H., Hilschmann N.;
"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. chymotryptic peptides of the H-chain, alignment of the tryp peptides and discussion of the complete structure.";
Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
5-SEP-2vv.
Ig heavy chain V-1.
Homo sapiens (Human).
Homo sapiens (Human).
Homo sapiens (Chaman).
Carla; Primates; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDILINE-77070267; PubMed-1002129; Dreker L., Schwarz J., Reichel W., Hilschmann N.; Dreker L., Schwarz J., Reichel W., Hilschmann N.; Reichel W., Hilschmann N.; In an an antibody structure. The primary structure of a monocloning of immunoglobulin (myeloma protein Nie), I: Purification and characterization of the protein, the L- and H-chains, the cyanogen bromide cleavage products, and the disulfide bridges."; Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976), Physiol. Chem. 357:1515-1540(1
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15-SEP-2003 (Rel. 42, Last annotation
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P01770;
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119
119 AA;
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76.7%;
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Pred. No. 9.8e
10; Mismatches
                       Craniata; Vo
Catarrhini;
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                                          Vertebrata; Euteleostomi;
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; 1g; 1.
R SMART; SM00406; IGv; 1.
R SMART; SM00406; IGv; 1.
Immunoglobulin v region; Pyrrolidone carboxylic acid.
M Immunoglobulin v region; Pyrrolidone CARBOXYLIC ACI
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01-JAN-1988
15-JUL-1999
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P06316;
                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                "Molecular cloning
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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"The switch point in mu heavy chains
Biochemistry 13:2482-2498(1974).
                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE-85062823; PubMed-6095199;
                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9606;
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01-JAN-1988 (Rel. 06, Last seq
15-JUL-1999 (Rel. 38, Last ann
Ig lambda chain V-I region BL2
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13166 MW;
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BL2 precurs
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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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Best Local S
Matches 86
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Pfam; PF00047; 1g; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin V region; Signification; Significa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV16_MOUSE
P01783;
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HSSP;
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NON_TER
SEQUENCE
                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a clear the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for
                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                           Adetugbo K., Milstein C., Secher D. "Molecular analysis of spontaneous Nature 265:299-304(1977).
                                                                                                                                                                                                                                                                                                                                                                                                             "Heavy chain variable region antibodies: somatic mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
DOMAIN
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GO; GO:0003823; F:antigen binding activity; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                  MEDLINE=77100368; PubMed=401950;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-81234548; PubMed-6788376;
Bothwell A.L.M., Paskind M., Reth M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 17-136.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Baltimore D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ig heavy chain V region MOPC 21
                                      ligc;
                                                      E90809; G1MS21
                                                                                                                                                                                                                                                                                                                                                                                             24:625-637(1981).
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                                                                             J00522; AAD15290.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLRGSVFGGGTKVTVLG 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GSWAQSVLTQPPSVSAAPGQKVTISCSGSSSNIGNDY-VSWYQQVPGTAPKLLIYDNNKR
IPR007110; I
IPR003006; I
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Rodentia;
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Pred. No. 3.6e
L5; Mismatches
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J SEGMENT.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                               contribution evident in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                                                                                                                                                                                              somatic mutants.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Imanishi-Kari T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                update)
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thi; Muridae; Murinae; Mus
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                                                                                                                                                                                          restrictions
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RESULT 8

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AC AC P06887

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AC P1- MI
AC P1- MI
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Best Local :
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GO; GO:0005576; C:extracellular; NAS
GO; GO:0003823; F:antigen binding act
GO; GO:0006955; P:immune response; NI
InterPro; IPRO07110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003906; Ig_WHC.
InterPro; IPR003906; Ig_V.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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NON_TER 1
SIGNAL <1
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01-JAN-1988
15-SEP-2003
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=85257662; PubMed=2410269;
Mihaesco E., Roy J.P., Congy N., Peran-Rivat L.,
"The amino acid sequence of a lambda light chain
physicochemical and antigenic features.";
Eur. J. Blochem. 150.349-357(1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR003599
Pfam; PF00047; ig;
SMART; SM00406; IG
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HSSP; P01703; 7FAB.
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DOMAIN
                                                                                 Pyrrolidone carboxylic acid.
DOMAIN 1 106
                                                                                                                    PROSITE; PS50835; IG_LIKI
Immunoglobulin V region;
                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 immunoglobulin-like
                                                                                                                                                                                                                                                                                                                                                                                      -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE
                                                                                                                                                                                                                                                                                                                                                                                                     -!- MISCELLANEOUS: RESIDUES 33-36 AND SOME WERE POSITIONED BY HOMOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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-JAN-1988 (Rel. 06, Last

-SEP-2003 (Rel. 42, Last

lambda chain V-I region
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Primates;
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D SEGMENT.
JH4 SEGMENT.
                                              PYRROLIDONE CABY SIMILARITY.
                                                                                   IG-LIKE
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         748124F079CFFBE4 CRC64
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RESULT 9
LV1D_HUMAN
LV1D_HUMAN
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Best Local Similarity
T_HUMAN
HV3T_HUMAN
P01781;
21-JUL-1986
21-JUL-1986
15-SEP-2003
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DISULFID
NON_TER
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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J. Blochem. 93:421-429(1983).
-!- SIMILARITY: Contains 1 immunoglobulin-like
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21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
15 lambda chain V-I region NIG-64.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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PYRROLIDONE CARBOXYLIC
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                                                                                                                                                                            P01767;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
15-SEP-2003 (Rel. 42, Last annotation
1g heavy chain V-III region BUT.
Homo sapiens (Human).
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Submitted (JUN-1975) to
"Complete amino acid sequence of the alpha 2 heav 19A2 immunoglobulin of the A2m (2) allotype."; Proc. Natl. Acad. Sci. U. S. A. 75:966-969(1978).
-i- MISCELLANEOUS: THE SEQUENCE OF THE ALPHA-2, A REGION OF THIS MYELOMA PROTEIN IS ALSO GIVEN.
-I- SIMILARITY: Contains 1 immunoglobulin-like dc PIR; A02059; A2HUBU.
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SMART; SM00406; IGv; 1.
SMART; PS50835; IG_LIKE;
Immunoglobulin V region.
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Mammalia; Eutheria;
NCBI_TaxID=9606;
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GO; GO:0003823; F:antigen binding activity;
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-ilke.
InterPro; IPR003596; Ig_MHC.
InterPro; IPR003596; Ig_V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Watanabe S., Barnikol H.U., Horn J., Bertram J., Hilschman "The primary structure of a monoclonal IgM-Immunoglobulin (macroglobulin Gal.), II: the amino acid sequence of the type), subgroup H III. Architecture of the complete IgM-m. Hoppe-Seyler's Z. Physiol. Chem. 354:1505-1509(1973).
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Mammalia; Eutheria;
                                                                                               MEDLINE=78137069; PubMed=416441; Torano A., Putnam F.W.;
                                                                                                                                                                                                                                                            HV3F_HUMAN
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HSSP; P01772; 2FB4.
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12730 MW;
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Primates;
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72.9%;
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                                                                                                                                                           Catarrhini;
                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                            PRT;
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HV3C_HUMAN
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Best Local S
Matches 84
InterPro; IPROU.
InterPro; IPROU.
InterPro; IPRO03596,
InterPro; IPRO03596,
IPRO0406; IGy; 1.
SMART; SMO0406; IGY; 1.
SMART; SMART; IGY; 1.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HV3C_HUMAN STANDARD; PRT; 117 AA. P01764; P1764; 21-JUL-1986 (Rel. 01, Created) 21-JUL-1986 (Rel. 01, Last sequence update) 15-SEP-2003 (Rel. 42, Last annotation update) 19 heavy chain V-III region VH26 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
                                                                                                                                                                                                                                  Genew; HGNC:5545; IGHV@.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity;
GO; GO:0003823; F:immune response; NAS.
GO:00006955; P:immune response; NAS.
InterPro; IPR003106; Ig_MHC.
InterPro; IPR003596; Ig_W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; J00236; AAA53516.1;
EMBL; M35415; AAA58735.1;
PIR; A02047; H3HU26.
PDB; 1HOU; 23-DEC-99.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matthyssens G., Rabbitts T.H.;
"Structure and multiplicity of genes for the human immheavy chain variable region.";
Proc. Natl. Acad. Sci. U.S.A. 77:6561-6565(1980).
-i- SIMILARITY: Contains 1 immunoglobulin-like domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; Immunoglobulin V region.
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SMART; SM00406; IGv; 1.
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InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
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12379 MW;
                                                                                                    Signal; 3D-structure.
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                             HEAVY CHAIN V-III REGION VH26
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RESULT 14 LV1F\_HUMAN

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GO; GO:0003823; F:antigen binding activity; NA
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig_1lke.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Bence-Jones protein;
Pyrrolidone carboxylic acid.
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Mammalia; Eutheria;
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6 (Rel. 01, Last :
3 (Rel. 42, Last :
                                                                                                                                                             Conservative
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Primates;
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                                                                                                                                                       13;
                                                                                                                                                                              Score 427.5;
Pred. No. 1.:
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PYRROLIDONE CARBOXYLIC
BY SIMILARITY.
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Pred. No. 9
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part of immunoglobulin L-chains of
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RESULT 15
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OS Homo s
OC Eukary
OC Mammal
OX NCBL_T
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RP SEQUEN
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RA Capra
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InterPro; IPN03590,
InterPro; IPR003590,
Pfam; PF00047; 1g; 1.
SMART; SM00406; IGv; 1.
SMART; SM00406; IGv; 1.
A PROSITE; PS50835; IG_LIKE; 1
Immunoglobulin v region.
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Matches
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                                                                MEDLINE-77117674; PubMed-65324;
Capra J.D., Hopper J.E.;
Capra J.D., Hopper J.E.;
"Comparative studies on monotypic IgM lambda and IgG kappa from an "Comparative studies on monotypic IgM lambda and IgG kappa from an Individual patient. III. The complete amino acid sequence of the V region of the IgM paraprotein."

Immunochemistry 13:995-999(1976).

-I- MISCELLANEOUS: THIS CHAIN WAS OBTAINED FROM IGM ISOLATED FROM OF THE WALDENSTROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
DISULFID
NON_TER
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21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Ig heavy chain V-III region BRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P04208;
20-MAR-1987 (Rel. 04, Created)
20-MAR-1987 (Rel. 04, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
19 lambda chain V-I region WAH.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Takahashi Y., Takahashi N., Tetaert D., Putnam F.N
"Complete covalent structure of a human immunoglol
the lambda light chain.";
Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690(1983).
PIR; A01967; L1HUMA.
HSSP, P01703; 7FAB.
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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     SIMILARITY: Contains 1; A02049; M3HUBW.
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GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding activity; NA
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR0077110; Ig-1ike.
R InterPro; IPR003006; Ig_MHC.
P InterPro; IPR003596; Ig_v.
ch completed: September
time: 12.6541 secs
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NON_TER
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE;
Immunoglobulin V region.
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                                                              100 ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARD-----
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120 AA; 13227 MW;
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Pred. No. 1.5e-24;
0; Mismatches 16
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Q925s1 mus
Q8wuk4 homo
Q8wtu6 homo
                                                      Q9u193
Q8wu38
Q8y509
Q9y184
Q9u184
Q8tc77
                                                                                                                                                     Q9u190
Q96e61
                  Q96bb9
Q9u171
                                                                                                                                                                                                                                                                     Q9qyf0 mus
Q921a6 mus
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## ALIGNMENTS

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RESULT 1

Q9QYPO
ID Y990Y
AC | Q90Y

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Best Local Similarity 64.0
Matches 185; Conservative
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Q9QYF0;
Q9QYF0;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2003 (TrEMBLrel. 23, L
CN 8 SCFV.
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InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03096; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 2.
PROSITE; PS50835; IG_LIKE; 2.
SEQUENCE 298 AA; 31867 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. 9
EMBL; AB036341; BA/
HSSP; P01607; 1REI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recognizing a cell polarity by using a phage display subtraction method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shinohara N., Demura T., Fukuda H.; "Isolation of a vascular cell wall-specific monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Balb/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
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MEDLINE=20183931; PubMed=10706631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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54.4%; Score 891; DB 11; 64.0%; Pred. No. 3.3e-59; Eive 29; Mismatches 67;
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Last sequence update)
Last annotation update)
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Best Loc
Matches
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X Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D N. Chung J.H., Choi I.H., Lee S.D N. Chung J.H., Chung H.K.;

A Y1 K.S., Suh P.G., Ryu S.H., Chung H.K.;

"Cloning and characterization of cDNAs encoding VH and VL of monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA generation of a single-chain Fv molecule (scFv).";

Hol. Cells 7:816-819(1997).

EMBL; U88067; AAB48044.1; -.

R InterPro; IPR003006; Ig_MHC.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR003596; Ig_v.

R Pfam; PF00047; 19; 2.
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Q921A6;
01-DEC-2001 (TrEMBLrel. 19, Cre
01-DEC-2001 (TrEMBLrel. 23, Las
01-MAR-2003 (TrEMBLrel. 23, Las
Anti-CEA 79 single chain Fv fra-
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; C:
Mammalia; Eutheria; Rodentia; S:
NCBI_TaxID-10090;
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                                                GSVFGGGTKV
                                                                                             GKGPRSAHTLHIYIQ----
                                                                                                                         GTAPK----LLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEADYYCQSYDSSLR
                                                                                                                                                                                                                                                                                           ADDFKGRFAFSLETSASTAYLQINNLKNEDTATYFCARKDLLRYFDYWGQGTTVTVSSGG
                                                                                                                                                                                                                                                                                                                    ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCARDRGYYYMDVWGKGTTVTVSSGG
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241 AA;
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50.8%;
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fragment (Fragment).
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Pred. No. 6.1e
33; Mismatches
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Submitted (DEC-2001) to the EMBL/GenBank/DDBJ da
EMBL; BCC020240; AAH20240.1; -.
InterPro; IPRO07110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; ig; 5.
SMART; SM00406; IGv; 1.
SMART; PF00040; IGV; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
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01-DEC-2001
01-DEC-2001
01-MAR-2003
 Cui D., 2
                                                  "Mechanism of exogenous nucleic acids and
the repair of intestinal epithelium after
World J. Gastroenterol. 6:709-717(2000).
[2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=10090;
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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Mammalia; Eutheria;
                                STRAIN-BALB/c;
                                                                                                                                                                         PubMed=11819679;
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Yan X.
e genes
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Rodentia;
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Primates;
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5; Mismatches
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                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Catarrhini;
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i; Hominidae;
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                                                                                                                                        Strausberg R.;
Submitted (DEC-2001) to the EM Submitted (DEC-2001) to the EM EMBL; BC020233; AAH20233.1; -.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2;
SMART; SM00406; IGV; 1.
PROSITE; PS00290; IG_MHC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPRO07110; Ig-like.
InterPro; IPRO03006; Ig_MHC.
InterPro; IPRO03596; Ig_v.
Pfam; PF00047; Ig; 2.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
NON_TER 218 218
SEQUENCE 218 AA; 23013 MW;
                                                                                                                                                                                                                                                                                                               Q8WUK4;
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the irrauiace
the same strain.
                                                                                                                                                                                                                                                                               Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
                                                                                                                          Hypothetical SEQUENCE 23
                                                                                                                                                                                                                                                                                                                                                          Q8WUK4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Int. J. Radiat. Biol. Relat. EMBL; AF240168; AAK43733.1;
                                                                                                                                                                                                                              TISSUE=Tonsil;
                                                                                                                                                                                                                                                                       Mammalia; Eutheria;
                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                     NCBI_TaxID-9606;
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QKPGQPPKLLIYAASKQGSGVPAGLLASGSGTDFSLNI 214
                                                                                                                                                                                                                                                                                                                                                                                                                              QLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAI 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAQVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNK
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                                                                                                                         l protein.
237 AA; 24897 MW;
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                                                                                                                                                                                                                                                                       Chordata;
Primates;
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                                                                                 Score 538.5; | Pred. No. 7.6e 5; Mismatches
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Pred. No. 2.7e-33;
0; Mismatches 62;
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                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                          73C7D70B8039D186 CRC64;
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                                                                                         .6e-33;
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                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                      DB 4;
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                                                                                  6,
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Q9UL90;
Q9UL90;
Q9UL90;
Q1-MAY-2000 (TrEMBLrel. 13, Created)
Q1-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Q1-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Q1-MAR-2003 (TrEMBLrel. 23, Last annotation variable)
Q1-MAR-2004 (Tremmunoglobulin heavy chain variable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q8WTU6;
Q8WTU6;
01-MAR-2002
PROSITE;
NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                               Clin.
EMBL;
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SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9614934;
MEDLINE=98277139; PubMed=9.L.,
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HSSP; P01772; 2FB4.
InterPro; IPR007110;
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InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003596; Ig_v.
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Submitted (JAN-2002)
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Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                    fetus.";
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                                                                                                                                                                                                                                                         Myosin-reactive autoantibodies in rheumatic
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                                           __rK003006; Ig_MHC.
__rC0; IPR003596; Ig_V.
m; PE00047; Ig; 1.
'T; SM00406; IGV.
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                                                                                                                                                                                                 Immunol. Immunopathol. 87:184-192(1998) AF035024; AAD56260.1; -.
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3 (TrEMBLrel. 23,
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ilarity 88.9%;
Conservative
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Last sequence update)
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Pred. No. 2.2e-32;
....matches 7;
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    ED57FDD19086D07F CRC64;
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Best Loc
Matches
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Submitted (AUG-2001) to the EMBL/GenBank/DDBJ da
EMBL; BC012876; AAH12876.1; -.
Interpro; IPR007110; Ig-1ike.
Interpro; IPR00306; Ig_MHC.
Interpro; IPR003596; Ig_V.
Pfam; PF00047; 1g; 2.
Pfam; PF00047; 1g; 2.
SMART; SM00406; IGV; 1.
PROSITE; PS05035; IG_LIKE; 2.
PROSITE; PS05035; IG_LIKE; 2.
PROSITE; PS05035; IG_MHC; 1.
PROSITE; PS05035; IG_MHC; 1.
PROSITE; PS05035; IG_LIKE; 2.

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Best Local (
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O9UL93; O1-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
                                                                                                           Young
                 SEQUENCE FROM N.A.
MEDLINE=98277139; PubMed=9614934;
Wu X., Liu B., Van der Merwe P.L.
                                                                                                      Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                               Myosin-reactive
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                       PSGVPDRFSGSKSGTSASLAITGLQAEDEADYYCQSYDGSLSGSVFGAGTKVTVLG
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                                                                                                                                                                                                         EMBLrel. 13, Last sequence update)
EMBLrel. 23, Last annotation update)
immunoglobulin heavy chain variable
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Primates;
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                       Merwe P.L.,
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Pred. No. 5.9e
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 508; DB Pred. No. 1.5e 6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
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Last annotation update)
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                                                                                                                            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7EC9FB3622FED957 CRC64;
                       Kalis
                                                                                                                                                                                                               chain variable
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.5e-30;
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                       N.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
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Best Local S
Matches 131
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Best Local
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ
EMBL; BC021276; AAH21276.1; -.
InterPro: IPR007111; Ig-like.
InterPro: IPR003006; Ig_MHC.
InterPro: IPR003056; Ig_WHC.
InterPro: IPR003596; Ig_V.
Pfam; PF00047; ig; 4.
SMART; SM00406; IOv; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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01-MAR-2002 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 573 AA; 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8WU38
                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS50835; IG_LIKE; 2. PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Tonsil;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 1. SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Myosin-reactive autoantibodies
fetus.";
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                                                                                                                            80
                                                                                                                                                                                                                                                                                               131;
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                                                                                                                                                                                                                                QVQLVQSGGGVVQPGRSLRLSCAASGFIFSSYGMHWVRQAPGKGLEWVAGIFYDGGNKYY
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                                                                                   TVSSGGGGSGGGGGGGSQSVLTQPPSV----SGA----PGQRVTISC--TGRSSNIGA
                                                                                                                                                                                                               EVQLVESGGGLVQPGRSLRLSCAASGFTFDDYAMHWVRQAPGKGLEWVSGISWNSGSIGY
                                               TVSSAP--
                                                                                                                              ADSVKGRFTISRDNAKNSLYLQMNSLRAEDTALYYCAKHGSGSYIGYYYGMDVWGQGTTV
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116 AA;
                                                                                                                                                                                                                                                                                            Conservative
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Primates;
      -QQLPGTAPKLLIYDDSNRPSGVPDRFSGSRSGTSASLAITGLQAEDEAD
                                                                                                                                                                                                                                                                                                                                                                                62967 MW;
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                                                                                                                                                                                                                                                                                                                  30.6%;
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Ig_MHC.
Ig_v.
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23,
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                                                                                                                                                                                                                                                                                               28;
                                                                                                                                                                                                                                                                                            Score 502; DB
Pred. No. 1.2e
28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
Last sequence update)
Last annotation update)
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                                               TKAPDVFPIISGCRHPKDNSPVVLACLITGYHP---T
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ches 13;
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...2e-29;
72;
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Best Local S
Matches 103
                                                Q9Y509;
01-NOV-1999
01-NOV-1999
01-MAR-2003
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InterPro;
     Homo sapiens (Human)
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96071149; PubMed-7475288;
Cao J., Vescio R.A., Rettig M.B., Hor
Lichtenstein A.K., Berenson J.R.;
"A CD10-positive subset of malignant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50835; IG_LIKE; 1
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InterPro; IPR003006; Ig_MH
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; S80860; AAD14339.1; -. HSSP; P01772; 2FB4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  myeloma using PCR with patient-specific immunoglobulin gene primers.";
Leukemia 9:1948-1953(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YYC -- QSYDSSLRGSVF --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SVTVTWYMGTQSQPQRTFPEIQRRD---
                                                                                                                                                                                                                                                                                                                                                                         LVTVSSAS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KKKEKEKEE
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  Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chordata;
Primates;
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Ig_MHC.
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23,
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Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 493; DB 4;
Pred. No. 1.1e-29;
0; Mismatches 22;
Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
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                                                                                                         region
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Best Local S
Matches 97
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01-JUN-2002
01-MAR-2003
                                                                                                                                                                                                                                                       Pfam; PF00047; 19; 4.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 4.
PROSITE; PS00290; IG_MHC; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Cl
Mammalia; Eutheria; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q8TC77
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NON_TER
SEQUENCE
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HSSP; P01772; 2FB4.
InterPro; IPR007110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-98277139; PubMed-9614934; Wu X., Liu B., Van der Merwe P.L.,
                                                                                                                                                                                                            Hypothetical protein. SEQUENCE 471 AA; 51791 MW;
                                                                                                                                                                                                                                                                                                                                                              EMBL; BC024289; AAH24289.1; 
Interpro; IPR0077110; Ig-like. 
Interpro; IPR003006; Ig_MHC. 
Interpro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Strausberg R.; Submitted (FEB-2002) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1.
SMART; SM00406; IGv; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young D.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fetus.";
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                                                                                                         97; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SS 157
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SS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR003006;
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                                                                                                         Conservative
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; AAD56266.1;
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23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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                                                                                                   Score 483; DB 4;
Pred. No. 2.6e-28;
3; Mismatches 35;
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.5e-29;
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Matches 95
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Q96BB9;
01-DEC-2001
01-DEC-2001
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Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BC015760; AAH15760.1; .
InterPro; IPR007110; Ig-like.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003506; Ig_v.
Pfam; PF00407; Ig; 5.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS50835; IG_LIKE; 5.
PROSITE; PS508290; IG_MHC; 3.
SEQUENCE FROM N.A.
MEDLINE-98277139; PubMed-9614934;
Wu X., Liu B., Van der Merwe P.L.
Young D.C.;
                                                                                                                    (Fragment).
(Fragment).
Homo sapiens (Human).
                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Myosin-reactive immunoglobulin heavy chain variable
                                                                                                                                                                                                                                                                                                                                                            Q9UL71
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SEQUENCE 59
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Homo sapiens (Human).
Eukaryota, Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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597 AA; 6
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(TrembLrel. 19, Last sequence update)
(TrembLrel. 23, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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73.1%;
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Pred. No. 3.8e
12; Mismatches
                      P.L.,
                                                                                                                                          Craniata; Vertebrata; Catarrhini; Hominidae;
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                      Kalis
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tches 16;
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                      Berney S.M.,
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Search completed: September Job time : 51.6122 secs
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NON_TER
SEQUENCE
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SMART; SM00406; IGV; 1.
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InterPro; IPR003596; Ig_v.
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InterPro; IPR003006;
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                                                                                                                                    121 S 121
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92; Conserv
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121 AA;
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76.0%;
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Pred. No. 1.8e-
10; Mismatches
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1.8e-28;
hes 16;
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